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October 28, 2003, 17:45:31; Search time 10243 Seconds (without alignments) 11652.371 Million cell updates/sec Run on:

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2888711 segs, 20454813386 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

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RESULT 1
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linear

DNA

Sequence 7 from Patent WO0233087. AX574596 AX574596.1 GI:27551852

Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens (human)

Edinger, S., Gerlach, V., Macdougall, J.R., Malyankar, U.M., Smithson, G., Millet, I., Peyman, J.A., Stone, D.J., Gunther, E., Ellerman, K., Shimkets, R.A., Padigaru, M., Guo, X., Patturajan, M.,

REFERENCE AUTHORS

VERSION AX574590.1 GI:27551849 KEYWORDS SOURCE Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhin; Hominidae; Homo. REPERENCE AUTHORS Smithson, G., Gerlach, V., Macdougall, J.R., Malyankar, U.M., Tallerman, K., Shimkets, R.A.; Padigaru, M., Guo, X., Patturajan, M., TITLE Gangolli, E.A.; Pernandes, E.R. and Gorman, L. Proferins and mucleic acids encoding same JOURNAL Patent: WO 0233087-A, 1 25-APR-2002; Cuzagen Corporation (US) FRATURES L. 2997 Mol. types "Gernonic DNA" Mol. types "Gernonic DNA" Abaref="teamonic DNA" Mol. types" "Gernonic DNA" Abaref="teamonic DNA" Mol. types" "Gernonic DNA" Mol. types "Gern	Query Match 92.4%; Score 2675.4; DB 6; Length 2997; Best Local Similarity 94.9%; Pred. No. 0; Anatches 2866; Conservative 0; Nismatches 5; Indels 150; Gaps 4; Oy 1 CGCTCCTGGATGAGCCCGGGGGGGCTTGGGGGGCTTGGGGATGCTG 60 Db 1 CGCTCCTGGATGAGCCGGGGGGGGGGGGGTTGGGGGGCTTGGGATGGTG 60			Qy 241 GCCTGGGAGCCCGAGCGCTCCTCCACCGGGGCGGCGGGCG	Qy 361 GAAAACCAAACACTGCATGTTCTCACTCAATATGACCTGCTCTGCCTACGAGGTTGAC 420 16	421	481	02	Qy 601 AAGACAGGACTAAAGTCTGTACGGCCAGAGGACTTCTGTTTCTATCAAGGC 660 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
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FEATURES Location/Qualifiers Source 1.5610 Acaptism="Homo sapiens" /mol type="genomic DNA" /bxref="taxon:9606" BASE COUNT 1233 a 1638 c 1537 g 1202 t ORIGIN	/ Match Local S nes 2289 202	Db 838 GCAGCACCTGCGTACGGCCATGGGCACCGCAGCGCAGCG	322	Oy 382 CTCACTCAATATGACCTGCTCTCTGCCTACGAGGTTGACCACAGGGGCGATTACCTGTCC 441 Db 945AATATGACCTGGTCTCTGCCTACGAGGTTGACCACAGGGGCGATTACGTGTCC 997	ON 442 CATGAAATCATGCACCATCAGCGGCGAAAAGAGCAGTGGCCGTGTCCCAGGTTGAGTCT 501	Oy 502 CTTCACCTTCGAAAGGCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGG 561	Oy 562 AGCCTAGTGGCTCCTGGCTTTATTGTGCAGAGCATGGGAAGACAGGCACTAAGTCTGTG 621	Qy 622 CAGACTTACCGCCACAGACTTCTATCAACGCTCTTTGCCATCACACACA	Qy 682 TGGCCATGGAGGGAAGTTCTGTGAGGCTCCACTGGCACTGGAAGCTCTGCAAC 741	Qy 742 AGTCAGAAATGTCCCCGGGACAGTGTTGACTTCCGTGCTGCTCAGTGTGCCGAGCACAAC 801	QY 802 AGCAGAGGTTCAGAGGGGGGCACTACAGTGGAAGCCTTACACTCAAGTAGAAGCCG 859	Oy 860 ACTYATGCAAACTCTACTGTATGGCAGAAGGATTTGATTT	OY 920 AAGTCAAAGATGGGACTCCATGCTCGGGGGATAGCCGTAATGTTTGTATAGATGGGATAT 979	980 GTGAGCTCAGTGCTCCATCTGC-GCACATGCCCCAGCCTCCCAAGAAACCTC	Db 1502 AAGCAGCATTTCTGTGGAAQACGCAAGAAATACACCCGAGCCTCCCAAGGAAGACCTC 1561 Ov 1019 TTCAACCTCACAAGACGATAAGTGTTAAGAGGAAAAGGGCTGTGTTGTGAGGTCC 1098	1562 TTCATCTTGCCAGATGAGTATAGGTTTACGGTAAGGGTTGTCTTCTGAGGTCT	Qy 1099 CATAGAAATGAAGAACTGAACGTOGAGACCTTGGTGGTGGTCGACAAAAAGATGATGCAA 1158
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TAKAHINO NAGASE, NOBIO NOMURA, KAZUHIRO YANO, KOJI MURAKAMI, SHINICHIRO YASUDA, KOJI KANZAKI

OS ALIÍFICIAL SEQUENCE

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PD 18-ARR-2001

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CSAMIOCHIRO YASUDA, KOJI KANZAKI

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Hunan proceases and polynucleotides encoding the Patent: US 6448388-A 3 10-SEP-2002;
Location/Qualifiers
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KEYWORDS WO 02051998-A/1. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (butter of sapiens by the sapiens	PP 21-002-2001 WO 2001JP011251 PR 21-DEC-2001 WO 2001JP011251 PR 22-DEC-2000 JP 00P 393372 PI NOBORU YAMAJI KOCHI NISHIMURA, KUNITAKE ABE, WAKOTO OCINO PC CI2NIS/09, COTKI6/40, CI2NS/10, CI2N9/50, GOIN33/15, GOIN33/50, PC GOINZ3/35/33/10, CI2NS/10, CI2NS/1	FT CDS (1). (3675). PERATURES 1. 3675 1. 3675 2. 3675	Garary Match 64.8%; Score 1874.6; DB 6; Length 3675; Best Local Similarity 84.4%; Pred. No. 0; Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;	QY 202 GCAGGCACCTGCGTGGGCCCATGGGACCCCAGGCGCCTGGGAGCCCCAGGCGTCCC 261 Db 69 GCAGGCACCTGCGTGGGCCCATGGGACCGCGAGCGCCTGGGAGCCCCGAGCGTCCC 128	QY 262 GCGTCCTCCACCCGGGGGGGGCGGCCGGGCTGGATGGATG	Oy 322	Oy 382 CTCACTCAATATGACCTGGTCTCTGCCTACGAGGTTGACCACAGGGGCGATTACGTGTCC 441	Qy 442 CATGABATCATGCACCATCAGCGGGGAGAAGAGCAGTGGCGTGTCCGAGGTTGAGTCT 501 Db 229 CATGABATCATGCACCATCAGCGGGGGAGAAGAGCAGTGGCCGTGTCCGAGGTTGAGTC 288	Qy 502 CTTCACCTTGGGCTGAAAGGCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGC 561 	562	622	Qy 682 TCGCCATCGCATGGAGGAAGTTCTGTGAGGGCTCCACTCGCAACCTTGCAAC
1693 CATGACATGTGGTGCCGGGGAGGACAGTGTGAAATATGGTGATGAAGGCCCCAAGCCC 1752 1873 ACCCATGGCCACTGGTCGACTGTCTTCTTGGTCCCATGCTCCAGGACTGCCGCAGGG 1932 1753 ACCCATGGCCACTGGTCGACTGGTCCACCCATGCTCCCAGGACTGCCGGAGGG 1812 1753 ACCCATGGCCACTGGTCGACTGGTCTTCTTGGTCCCCATGCTCCAGGACTGCCGAGGGACTGCGGAGGGGGGGG	2053 GTTGACTTTCCGTGCTCACTCGTGCTGCCGACACAACAACAACAACAACAACAACAACAACAACAA	QV 2173 GCAGAAGGATTGATTCTTTTTTTTTTTTTTTTTTTTTTT	2293 GICCITIGGANCHGATGCTGTTGAAGACGTCTGTGGGGGTGTGTAACGGGAATAACTCAGCC 		Oy 2413 GTCACCATTCCTTCTGGAGCCCGGGAGTATCGGCATCTATGAAATGAACGTCTCTACCTCC 2472 [QY 2473 TACATTTCTGTGCGCAATGCCCTCAGAAGGTACTACCTGAATGGGCACCGTGGAC 2532 Db 2353 TACATTTCTGTGCGCAATGCCCTCAGAAGGTACTACCTGAATGGCCATGGACCGGGGAC 2412	QY 2533 TOSCCCOGCCGGTACAAATTTTCGGCCACTACTTTCGACTACACACGCTCCTATAATGAG 2592 Db 1	QY 2593 CCCGAGAACTTAATGGCTACTGGACCAACGAGACACTGATTGTGGGGGCTGCTTT 2652 Db 2473 CCCGAGAACTTAATGGCTACTGGACCAACCAACGAGACACTGATTGTGGAGCTGCTGTTT 2532	Qy 2653 CAGGGBAGCAGCCGGGTCTTGCCTGGGATACTCCATGCCTCGGGACCGAGAAG 2712	Qy 2713 CAGCCCCTGCCCAGCTACACTTGGGCCATCGTGTCTCTGAGTGCTCCGTGTCC 2772 Db 2593 CAGCCCCTGCCCAGCCAGCTACACTTGGGCCATCGTGCGCTCTGAGTGCTCCGGTGTCC 2652	Qy 2773 TGCGGAGGGG 2783 	RESULT 9 BD170564 BD170564 LOCUS LOCUS DEFINITION Novel procease. ACCESSION BD170564 UG121876376

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EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE AUTHORS AUTHORS Edinger, S., Gerlach, V., Macdougall, J.R., Malyankar, U.M., Smithson, G., Millet, I., Peyman, J.A., Stone, D.J., Gunther, E., Ellerman, K., Shimhets, R.A., Padigaru, M., Guo, X., Patturajan, M., Taugier, R.J., Burgess, C.E., Zerhusen, B.D., Kekuda, R., Spytek, K.A., TITLE JOURNAL Patent: WO 0233087-A 3 25-APR-2002; Curagen Corporation (US) FEATURES 10.2431/Qualifiers JOURNAL Patent: WO 0233087-A 3 25-APR-2002; Curagen Corporation (US) FEATURES 10.2431/Qualifiers JOURNAL MODERAL MODERAL MAN MODERAL M	Query Match 62.0%; Score 1785.6; DB 6; Length 2433; Best Local Similarity 82.0%; Pred. No. 0; 34; Indels 489; Gaps 7; Matches 2375; Conservative 0; Mismatches 34; Indels 489; Gaps 7; Qy 1 CGCTCCTGGATGAAGCCCGGGGGGGGGGGGGGGGGGGGG	Oy	181 GCGATGTCGCCGCTGTTTTCCGCAGGCACCTGCGTGCGCCATGGGACCCGCAGCGGCAGC 240	Qy 301 AAAGGGGGGACATGGATGAAGCTGGAAACCATCGTTCTCAGCAAACTAACACAGGAACA 360 Bb 322 AAAGGGGGGACATGGATGGAAGCTGGATCTCAGCAACTAACAGGAACA 381 Qy 361 GAAAACCAAACATGCATCTCACTCACAACAGGAACA 381 Db 382 GAAAACCAAACACGGATGTTCTCACTCAAATATGACCTGGCTACCAGAGGTT 417 Db 382 GAAAACCAAACACTGCATGTTCTCACTCATCATATATGACCTGGTCTCTGCCTACGAGGTT 441	Qy 418 GACCACAGGGGCGATTACGTGTCCCATGAAATCATGCACCATCAGCGGGGGAGAAGGACA 477 Db 442 GACCACAGGGGGCGATTACGTGTCCCTTGGAAATCATGCGGCGGGGGGGG	Db 502 GTGGCCGTGGCGAGGTTGAGTCTCTTCACCTTCGGCTGAAAGGCCCCAGGCACTC 561 Qy 538 CACATGGATCTGAGACTTCCACCCTAGTGGCTCTGGCTTTTTTTT	Qy 598 GGAAAGACACTAAAGTCTGTGCAGACTTTACCGCCAGAGACTTTTCTATTCTATCTA
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	Taupier R.J., Burgess, C.E., Zerhusen, B.D., Kekuda, R., Spytek, K.A., Gangolli, E.A., Fernandes, E. B. LE Proteins and nucleic acids encoding same. RNAL Patent: WO 0233087-A 52-APR-2002; RES Location/Qualifiers source /organism="Homo sapiens" /mol type="genomic DA" /mol type="genomic DA" /db xref="taxon:9606" Odery Match S8.5%; Score 1695; DB 6; Length 2902;	100 CACCAGGGGGGAAACCGGGGGTCCGGAACAGCTGGAGGGAAGTCCCCGCGGGTCCTCTCC 159	220 CATGGGACCCCCAGCGGCAGCGCTGGAAGCCCCGAGCGTCCCCGCTCCTCCTCCCCCCCC	340 CAGCAAACTAACACAGAACAGAAACCAAACACTGCATGTTCTCACTCA	460 CACCGGCGGAAGAGCAGTGGCCGTGTCCGAGGTTGAGTCTCTTCACCTTCGGCTGAAA 519	
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	1724 AGGACATCTGTAAAGCCCTGTGCTGATTGGAAGGAATTGTGAAGCTAAATTTA 1783

	1544 GCGGCGAGTATCTAACACACACTCACCGCTCAACATATTGCTAGGTACTACG 1603		1664 ACACAGRICCAAGTIGCAGTICGAAGAGAAGCAACTICTGCATGCTGCAGTTTAAAA 1723 	1724 AGGACATCTGTAAAGCCCTGTGGTGCCATCGTATTGGAAGGAA	1784 TGCCAGCAGCAGAAGGCACAATTTGTGGGCATGACATGTGGTGCCGGGAGGACACAGTGTG 1843 		GGTCCCCANGCTCCAGGACTGCGGAGGGGGGGGTATCTCATAGGAGTCGCCTCTGCACCA	1177 GGTCCCCATGCTCCAGGACCTGCGGAGGGGGGAGTATCTCATAGGAGTCGCCTCTGCACCA 1236 1644 BCCCCCATGACCATGAAGGTAGTTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCT 2023		2024 GEARGAGTORANIGTCCCCGGARAGTGTGAGTTGCGTGGTGGTGGTGGGGC 2083 1297 GEARCAGTGGCAAATGTCCCCGGGARCAGTGGTCCTGCTGCTGGTGGTGGGGGGGGG 1356	2084 ACAACAGGAGGATTCAGAGGGGGGCACTACAAGTGGAAGCCTTACACTCAAGTAGAAG 2143	2144 ATCAGGACTTATGCAAACTCTACTGTATGGGAGAAAGATTTCTTTC	2204 CAAATAAAGTCAAAGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGTATAGATG 2263			Grossfergerandsgehalten (1997)			2504 ACTACCTGAATGGGCACTGGACGGTGGACTGGCCCGGCGGTACAATTTTCGGGCACTA 2563 1777 ACTACCTGAATGGGCACTGGACTGGCCCGGCGGGCGGGTACAATTTTCGGGCACTA 1836
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		Description	Human ADAM-TS 7-11	Human zinc matallo	Human metalloprote	Human con encodin	Plasmid pPastBac1-	Plasmid peastBact-	Human MDTS9 protea	Novel human protea
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Human; NOVX; cardiomyopathy; atherosclerosis; cell signal processing; breast cancer; Alzheimer's disease; epilepsy; Huminingcon's disease; RW anxiety; behavioural disorder; multiple sclerosis; mysathenia gravis; KW anxiety; behavioural disorder; multiple sclerosis; mysathenia gravis; KW anxiety; behavioural disorder; multiple sclerosis; mysathenia gravis; MW autonomeune disease; allergy; addiction; asthma; transplantation; graft versus host disease; MY infection; human immunodeficiency virus; MSW graft versus sciences; systemic lupus erythematosus; scleroderma; psoriabls; Crohn's disease; MY infection; human immunodeficiency virus; thromboycopoemia; bheeding disorder; metholic disorder; obscipty; My glucose transport defect; glomerulonephritis; hypercalcaemia; hypercaese; hypercaes; howth disorder; resproductive disorder; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; howth; hypercaes; hypercaes; howth; hypercaes; hypercaes; hypercaes; howth; hypercaes; hyperc

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ALIGNMENTS

ABS59326 standard; DNA; 2895 BP

ABS59326

ABS59326;

Human ADAM-TS 7-like gene #2. 05-NOV-2002 (first entry)

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17-CCT-2000; 2000US-241058P

17-CCT-2000; 2000US-241058P

17-CCT-2000; 2000US-241152P

23-CCT-2000; 2000US-241152P

23-CCT-2000; 2000US-24812P

23-CCT-2000; 2000US-24812P

24-CCT-2000; 2000US-24881P

24-CCT-2000; 2000US-24881P

25-FAR-2001; 2001US-24381P

26-FBB-2001; 2001US-24381P

26-FBB-2001; 2001US-24381P

29-FAR-2001; 2001US-286324P

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16-OCT-2001; 2001US-0981151
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P-PSDB; ABG76897.
                   WO200233087-A2.
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Padigaru M, G
Zerhusen BD,
       Homo sapiens
                                   25-APR-2002
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Gerlach V, MacDougall JR, Malyankar UM, Swithson G; Peyman JA, Stone DJ, Gunther E, Ellocran K, Shimkets RA, Ouo X, Patturajan M, Taupier RJ, Burgess CE, D, Kekuda R, Spytek KA, Gangolli EA, Fernandes ER;

Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheimer's disease, cardowyopathy, metabolic disease and

Claim 8; Page 19; 305pp; English.

The present invention relates to new NOVX (NOV1-10) polypeptides. The molecules of the invention are useful for treating or preventing a molecules of the invention are useful for treating or preventing a disorder related to cell signal processing and metabolic pathway modulation in humans. NOYX polypeptides, nuclaic acids and antibodies are useful for treating or preventing disorders or syndromes including breast cancer, Altahimmer's disease, epilepsy, Huntingron's disease, anxiety, behavioural disorders, multiple sclerosis, mysthemia gravis, neurodegeneration, Parkinson's disease, pain, stroke, autoimmune disease, allargise, addiction, asthma, endometriosis, graft versus host disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial and disease, laterial di

Sequence 2895 BP; 699 A; 760 C; 787 G; 649 T; 0 other;

ö Gaps 100.0%; Score 2895; DB 24; Length 2895; 100.0%; Pred. No. 0; tive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 2895; Conservative Query Match

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g è	121 TCC	JOSACASCTIGGAGGGAGTCCCCCGGGGGTCCTCTCCCGGGGGCCCCGCCGTCTCACC 180 NATION CACCGCTGTTTTTCCGCAGGAACAACAACAAGGGCCCCAAGGGAACACAAGAAG
7 A	181 GCG	ANTORCOCCOCTOTITICCOCAGGGCACCTGGGGGCGCCATGGGACCCGCAGCGCGCAGC 240
හි සි	241 GCC	GCTGGGAGCCCGAGCGTCCCGCGTCCTCCACCGGGAGCGGCCGGGCTGGATGGA
ìè	301 AAA	GGGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
7 A	301	NGGGGGGGACACAGATGATGTTCTTCACAAACACAGAACA 360
8	361 GAP	AAACCAAACACTGCATGTTCTCACTCAATATGACCTGGTCTCTGCCTAGGTTGTGAC 420
qa	-	CABACACTGCATGTTCTCACTCAATATGACCTGGTCTCTGCCTACGAGGTTGAC
දු දු	421 CAC	SGGCGATTACGTCTCCCATGAAATCATGCACCATCAGCGGCGGGGAGAACAGCAGTG
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δ	541 ATC	TGAGGACTTCCAGCAGCCTAGTGGCTCCTGGCTTTATTGTGCAGACGTTGGGA
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윱	***	3GCACTAAGTCTGTGCAGACTTTACCGCCAGAGGACTTCTGTTTCTATCAAGGC
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ò	1021 CCT	CCCAAGGAAGACCTCTTCATCTTGCCAGATGAGTATAAGTCTTGCTTACGGCATAAG 108
ପ୍ର	1021 CCT	cccaaggaccrcrrcarcrrgccagargagraraagrcrrgcgcaraag

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	0y 2401	Qy 2581 TOCTATAATGACCCGAGAACTTAATGGACCAACCAACCAACC	Qy 2761 TGCTCGGTGTCCTGCGGAGGGGTAGGTGCCTTCCAGGGGTGTCTCCTGGAGGTGTCTCCTGGAGGTGTCTCTGTGTTCTTCTTGTTTTTTTT	RESULT 2 ABS59323 ID ABS59323 ID ABS59323 standard; DNA; 2997 BP. XX AC ABS59323; DT GS-NOV-2002 (first entry) XX WHATHOUS TO COMMENT OF A STANDARD STAND
1081 CGCTCTTCTGAGGTCCCATAGAAATGAAGAACTGAACGTGGAGACCTTGGTGGTGGTC	ACTITIGGGATTICCACCCATAAGTGGAATGTGTAGTAAATATCGCAGCTGGAGGATTAAT	ATCATTCTAAGCACGAAGCAACATCTCTCCTCGTCACCCAACACAACATCATGTCCCCCCCC	1621 TACAAGTATCCTGAGAAATTGCCGGGGAGAATTATATGAGAAACAACACACAGTGG 1880 1681 CAGTTCGGAGAAAAGCCAGCCTGCATCTGAACTTTAAAAAGGACACTTGTAAGCC 7740 1681 CAGTTCGGAGAAAACCAAGCTTGCATGCATTTAAAAAGGACATCTGTAAAAGCC 7740 1741 CTGTGGTGCCATCGTATGGAAGCAAATTGTGAGACTTTATGCCAGCAGAAGCC 1800 1741 CTGTGGTGCCATCGTATGGAAAGTGTGAGACTAAATTATGCCAGCAGAAGGC 1800 1741 CTGTGGTGCCATCGTATGGAAGGAAATTGTGAGACTAAATTATGCCAGCAGAAGGC 1800 1801 ACAATTGTGGACATGAAAGGAAATGCAGAAGACTGTAAATTATGCCAGCAGAAGGC 1800 1801 ACAATTGTGGACATGAAATGCAGGAAGAACATGTGTGAAATATGGTGATGAA 1860 1801 ACAATTGTGGGCATGAAATGCAGGAGGAACAGTGTGTGAAAATTATGCTGATGAA 1860	1861 GOCCCCAAGCCCACGCACGCACGCACGCACCCATCTCTTGCTCCCCATGCTCCCAGG 1920 1861 GOCCCCAAGCCCACGCACGCCAGGCCACGCACCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCAGGCCCCAGGCCACCCCAGGCCACCCCAGGCCACGCCACCCCAGGCCATCCCAGGCACGCAC

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muscle disorder; bone disorder; joint disorder; skeletal disorder; haamatopoietic disorder; ottomary system disorder; osteroporosis; ds; dental disease; dental infection; growth disorder; reproductive disorder; hypogonadism; fertility disorder; viral infection; parasitic infection; parasitic infection; parasitic infection; parasitic infection; metabolic pathway modulation; gene therapy; gene; zinc metalloporotase; ADAM TS 7; alpha 2-macoglobulin precursor; ileal sodium/bile acid cortansporter; prohibitin; MT; CIP4; spinesh; macrophage stimulating protein; precursor; fatty acid-binding protein; application beta 5 protein; hepsin/plasma transmembrane serine protease; single mucleoide polymorphism; SNR. gastro-intestinal disease; congenital diarrhoea; respiratory disease;

Homo sapiens.

replace (481,C) /*tag= b /standard_name= "Single nucleotide polymorphism (SNP)" /*tag= a /standard_name= "Single nucleotide polymorphism (SNP)" /standard_name= "Single nucleotide polymorphism (SNP)" name= "Single nucleotide polymorphism (SNP)" *tag= e standard_name= "Single nucleotide polymorphism (SNP)" Location/Qualifiers replace (472,G) replace (1121,C) replace (1566,C) /*tag= d /standard r O variation variation variation variation variation

17-OCT-2001; 2001WO-US32496

17-OCT-2000; 2000US-241040P.
17-OCT-2000; 2000US-2410588.
17-OCT-2000; 2000US-241249.
20-OCT-2000; 2000US-241249.
23-OCT-2000; 2000US-242418.
23-OCT-2000; 2000US-242881.
23-OCT-2000; 2000US-242881.
23-OCT-2000; 2000US-242881.
24-OCT-2000; 2000US-242881.
25-DEC-2000; 2000US-242881.
25-DEC-2000; 2000US-242881.
25-DEC-2000; 2000US-242881.
25-ACT-2000; 2000US-242881.
26-ACT-2000; 2000US-242881.
27-ACT-2000; 2000US-242881.
28-ACT-2000; 2000US-242881.
28-ACT-2000; 2000US-242881.
29-ACT-2000; 2000US-242881.

CURA-) CURAGEN CORP.

Gerlach V, MacDougall JR, Malyankar UM, Smithson G; Peyman JA, Stone DJ, Gunther E, Ellerman K, Shimkets RA; Guo X, Patturajan M, Taupier RJ, Burgess CE; D, Kekuda R, Spyrek KA, Gangolli BA, Fernandes ER; Padigaru M, C Zerhusen BD, Edinger S, Gorman L;

WPI; 2002-590434/63. P-PSDB; ABG76894.

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AAGACAGGCACTAAGTCTGTGCAGACTTTACCGCCAGAGGACTTCTGTTTCTATCAAGGC

ATGGATCTGAGGACTTCCAGCAGCCTAGTGGCTCCTGGCTTTATTGTGCAGACGTTGGGA

541 541

GCCGTGTCCGAGGTTGAGTCTTCACCTTCGGCTGAAAGGCCCCCAGGCACGACTTCCAC

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and Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheimer's disease, cardiomyopathy, metabolic disease diabetes.

Claim 8; Page 12; 305pp; English

The present invention relates to new NOVX (NOV1-10) polypeptides. The

MONY-associated disorder, usus cardiomyopathy, atherosclerosis, or a disorder related to cell signal processing and metabolic pathway a disorder related to cell signal processing and metabolic pathway modulation in humans. Movy polypeptides, nucleic acids and antibodies are useful for treating or preventing disorders or syndromes including breast cancer. Altahamer's disease, epilepsy, Huntington's disease, anxiety, behaviouxal disorders, multiple sclerosis, myschenia gravis, neurodegeneration, parkinson's disease, pain, stroke, autoimmune host disease, allergies, addiction stream, endometriosis, graft versus host disease, allergies, rheumatods, scleroderma, transplantation, psorhasis, cronn's disease, HUN Human immunodeficiency vixus) infection, psorhasis, cronns disease, HUN Human immunodeficiency vixus) infection, clinose transport defect, glomerulomephritis, hypercalcaemia, polycystic clinose transport defect, glomerulomephritis, hypercalcaemia, polycystic clines disarboe, respiratory disease, gastro-intestinal diseases, compental disarboe, respiratory disease, gastro-intestinal diseases, curinary system disorders, osteoporosis, dental disease and infection, growth and reproductive disorders, hypogenadism, fertility, and/or other curinary system disorders, viral, bacterial, or parasitic infections. Therefore the present mucleic acid sequence encodes a NOVX protein of the Sequence 2997 BP; 728 A; 783 C; 809 G; 673 T; 4 other; useful for treating molecules of the invention are

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92.4%; Score 2675.4; DB 24; Length 2997;

Bart Local Similarity 94.9%; Pred. No. 0;

Marches 2866; Conservative 0; Mismatches 5; Indels 150: 0

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        tool for a disease
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                                                                                                                                                   0; Mismatches 177; Indels 245; Gaps
                                                                                                                DB 24; Length 3675;
                     disorder such as those above. AAS97159-AAS97195 represent human protease coding sequences and primers of the invention.
                                                                            Sequence 3675 BP; 874 A; 1009 C; 1019 G; 773 T; 0 other
      disorders. (I) may also be useful as a diagnostic
                                                                                                             Query Match 64.9%; Score 1877.8; Best Local Similarity 84.4%; Pred. No. 0; Matches 2289; Conservative 0; Mismatches
                                                                                                         Query Match
Best Local Similarity
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                                                                                                         GCATGTCAGCCTTCAGCCACTGCGTACATTGCACTGGCCTTTCTTGAATCCTAATGAGCA 2874
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; protease, PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigratine; analgesic; endocrine; noctropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antiminamatory; aspartyl protease; cysteine protease; anorectic; antiminamatory; aspartyl protease; cysteine protease; new teallogorease; anofesi, hemantopolicit; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney, pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mod disorder; attention disorder; cognition disorder; proteinsion; hypertension; psychotic disorder; dyskinesia, metabolic disorder; inflammatory disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated, enriched, or purified procease polypeptide (I) and polymelecide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering s (which modulates procease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoletic origin, of the breast, colon, lung, prostrate, cervical, disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, neurolajical disorders, hypotension, hypotension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   may
                                     TCTGAGTGCTCCGTGTCCTGCGGAGGGGGTAGGTGCCTTCCAGTGCTGCTCCTGGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel procease polypeptide useful for screening for substances that be used to treat, e.g., cancers; immure-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory cardiovascular disease, migraine, pain, psychotic and inflammatory
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                                                                                                                                                                                  GCCCGGGGCTTCTCCCTGCCA
                                                                                                                                                                                                                                                                                                        AAS97174 Standard, cDNA; 3675
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Human brain-originated ADAMTS family polypeptide and encoded gene, applicable in diagnosits and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
                                                                                                                              /standard_name= "Single_nuclectide_polymorphism"
replace (1620,A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 135-145; 172pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                        (KAZU-) KAZUSA DNA RES INST FOUND.
(MITS-) MITSUBISHI PHARMA CORP.
product= "ADAMTS'
                                                           replace (1079,T)
                                                                                                    replace (1097,G)
                replace (821,T)
                                                                                                                                                                                                                                                                                                                11-OCT-2001; 2001WO-JP08913
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Kanzaki K;
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                                                                                                                                                                262 GCGTCCTCCTCCACCCGCGGAGCGGCCGGGCTGGAAAAGGGCGGGACATGGATGAA 321
                                                                                                                                                                                                                                                322 GCTGGAAACCATCGTTCTCAGCAAACTAACAGGAACAGAAAACCAAACACTGCATGTT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                  1622 CATAGAATGAACTGAACGTGGAGACCTTGGTGGTGGTGGTCGACAAAAGAAGTGGTGCAA
                                                                                                                        838 scadecaccrecereceratescarececacecacacaccacececerescarececeaececeaececeaecece
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                                                                                  202 GCAGGCACCTGCGTGCGCCATGGGACCCGCAGCGCCAGCGCCTGGGAGCCCGAGCGTCCC
                                                                                                                                                                                                        898 GCGTCCTCCTCCACCCGCGGGCGGCCGGCTGGATGGAAAAGGGCG------
                                                                                                                                                                                                                                                                                                                              382 CTCACTCAATATGACCTGGTCTCTGCCTACGAGGTTGACCACAGGGGCGATTACGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                              CATGAAATCATGCACCATCAGCGGCGGAGAGAGCAGTGGCCGTGTCCGAGGTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCACCTTCGGCTGAAAGGCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGC
Query Match 64.9%; Score 1877.8; DB 24; Length 5610; Best Local Similarity 84.4%; Pred. No. 0; Matches 2289; Conservative 0; Mismatches 177; Indels 245; Gaps
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	2942 GTCCTTGGATCTGCTGTTGAGACGTCTGTGGGGGGTGTGTAGGGGGATTGAGCGGGATTGAGCCAGCGAGCG	2413 GTCACCATTCCTTCTGGAGCCCGGAGTACCGCATCTATGAATGA	2473 TACATTYCTG10-00-CATTCCTCACAAGGTACTACTGACAGGCACTGCACCCTGCACCTGCACCGAATGCGCAATGCGCAATGCCCTCACAATGCGCACTGCACCGCAATGCGCCCTCACAATGCGCACTGCACCGCACCGCACCGCACCGCACCGCACCGAATGCGCACTGCACCAC	2533 TGGCCGGGCGGTACAAATTTTCGGGCACTACTTCGACTACAACGGCCGGTACAATGAG \$1181 TGGCCCGGCCGGTACAAATTTTCGGGCACTACTATCGACTACAGACGGTCCTATAATGAG	2593 CCGGAGACTIAATGGCTACTGGACCAACGAGGAGCACTGATTGTGGAGCTGCTGTTT [[2653 CAGGRAAGGAACCCGGGTGTTGCCTGGGAATACTCCATGCCTCGCTTGGGGACCGAGAG 	2713 CAGCCCCTGC 	Qy 2773 TGCGGAGGGG 2783 Db 3422 TGCGGAGGGG 3432	RESULT 5 ABK49825 ID ABK49825 standard; DNA; 8435 BP.	XX		<pre>KW antiarthritic, antialcer; vulnerary; neovascularisation; angiona; KW diabetic omentopathy; chronic rheumatoid arthritis; gene therapy; KW refractory skin ulcer; generic ulcer; post-operative healing failure; KW reprolysin-type ZN-metalloprotease domain; disintegrin-like domain; 7SP1;</pre>		OS Homo sapiens. OS Escherichia coli. OS Baculovirus. OS Rhesus macaque polyoma virus.		XX PD 18-APR-2002. XX
	1862 TTCTGCCAGTGGCAGTCGATTGATGGGAAAGATGGACTCGTCATCACCAGCCATC 1921 1273 TTACTGACTGGTCTGGATATATTCCTGGAAAGAGGACCTGGACACTTTGGGATT 1332 1922 TTACTGACTGGTCTGGATATATTCTCTGGAAGAATGAGCCCTGTGACACTTTGGGATT 1332 1922 TTACTGACTGGTCTGGATATATGTTCCTGGAAGAATGAGCCCTGTGACACTTTGGGATT 1981	1333 GCACCCATAAGTGGAATGTGTAGTAAATATCGGAGCTGCACGATTAATGAAGATACAGGT 1392 	1393 CTTGGACTGGCCTTCACCATGCCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT 1452	1453 GGAGAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATCCCCTACATTGGCAGGA 1512 	1513 GGCAATGGAGTCTTCTCTGGTCACCTGCAGCGCCAGTATCTACACAATTTCTAAGC 1572 	1573 ACCGCTCAAGCTATCTGCCTTGCTGATCAGCCAAGCCTGTGAAGGAATACAAGTATCCT 1632 	1633 GAGAAATTGCCAGGAGAATTATATGATGCAAACACAGTGCAAGTGGCAGTTGGGAGAG 1692 	1693 AAAGCCAAGCTCGGATGCTGGACTTTAAAAAGGACATCTGTAAAGCCCTGTGGTGGCCAT 1752 	1753 CGTATTGGAAAGSAAAGGGAGACTAAAGTTANGCCAGCAGGAGAGAGACACAATTGGGG 1812 	1813 CHTGACATGTGCCCGGGGAGACAGTGTGTGAAATATGGTGATGAGGCCCCAAGCCC 1872 	1873 ACCATGOCCACHGGNCGGACTGGTCTTCTTGGTCCCCATGCTCCAGGACCTGCGGAGGG 1932	1933 GGAGTATCTCATAGGAGTCGCCTCTGCACCAACCCCAAGCCATGGCATGGAGGGAAGTTC 1992 	1993 TOTGAGOGETCCACTCGCACTCTGAAGCTCTGCAACACTCAGAAATGTCCCCGGGACAGT 2052 	2053 GTTGACTTCCGTGCTGAGTGTGCCGAGGACAACAAGAGAGAG	2113 TACAAGTGGAAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATC 2172 	2173 GCROAAGGATTGATTCTTTTTTTTTTTAAAAAAGGAGAGGGACTCCATGC 2232
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Human brain-originated ADAWTS family polypeptide and encoded gene, applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
                                                       Nagase T, Nomura N, Yano K, Murakami K,
                                                                                                                         Example 20; Page 155-159; 172pp; Japanese.
                                  (KAZU-) KAZUSA DNA RES INST FOUND. (MITS-) MITSUBISHI PHARMA CORP.
11-OCT-2001; 2001WO-JP08913.
            11-OCT-2000; 2000JP-0311309.
02-APR-2001; 2001JP-0102905.
                                                                              PI; 2002-372277/40.
                                                               Kanzaki K;
                                                          Ohara O.
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The invention relates to a polypeptide belonging to the ADAMYS family is selected from sequences appearing as AAD19466, AAD19491 and AAD19499.

selected from sequences appearing as AAD19466, AAD19491 and AAD19499.

Compared to the contains the polypeptide, a protein having not less than polypeptide modified from any of the polypeptides but with some amino cid sequence of the polypeptides but with some amino cid sequence of the polypeptides or a mino cid sequence of the polypeptides but with some amino cid sequence of the polypeptides but with some amino cid sequence or the polypeptide but with some and polypeptides or variants, a recombinant vector containing any of the polypeptide, protein or populate the polypeptide, protein or peptide and screening compounds to promote or inhibit expression of the polypeptide, protein or peptide and screening compounds to promote or inhibit expression of the polypeptide protein, peptide and screening compound for context before evaluating the polypeptide protein, peptide and encoded gene collypeptide by using the polypeptide protein, peptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes. The polypeptide and encoded gene activity by measuring signal changes and screening compound to contain and gastric ulcers and post-operative healing signal changes including such polypeptide has conserved reprolosity. Activity of the gene on the spending and decrease in tumour cell and location of the gene on the spending cha

Sequence 8435 BP; 2072 A; 2174 C; 2149 G; 2040 T; 0 other;

	6;	261	4179	321	4226	381	4226	441	4279	501
** **	Matches 2289; Conservative 0; Mismatches 177; Indels 245; Gaps	202 GCAGGCACCTGCGTGCGCCATGGGACCCGCAGCGCCAGCGCCTGGGAGCCCGAGCGTCCC 261	4120 GCAGGCACCTGCGTGCGCCATGGGACCCGCAGCGCCGCTGGCAGCCCCGAGCGTCCC 4179	262 GCGTCCTCCTCCACCCGCGGAGCGGGCTGGATGGAAAAGGCGGGACATGGATGAA 321	4180 GCGTCCTCCACCCGCGGAGCGGCCGGCCTGGATGGAAAAGGGCG 4226	322 GCTGGAAACCATCGTTCTCAGCAAACTAACACAGGAACAGAAAAACCAAACACTGCATGTT 381		382 CTCACTCAATATGACCTGGTCTCTGCCTACGAGGTTGACCACAGGGGGGGATTACGTGTCC 441	4227AATATGACCTGGTCTCTGCCTACGAGGTTGACCAGGGGGGGATTACGTGTCC 4279	442 CATGARATCATGCACCATCAGCGGGGGAGAAGAGCAGTGGCCGTGFCCGAGGTTGAGTT 501
uery Match	atches 2289	202	4120	262	4180	322	4227	382	4227	442
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4460 CAGACTITACCGCCAGAGGACTTCTGTTTCTATCAAGGCTCTTTGCGATCACACAGAAAC 4519 4556 GGCATGÁTACGAACAGAAGAGGCAGATTÁCTTCCTAAGGCCACTTCCTTCACACCTCTCA 4615 980 GTGAGCTCAGTGTGGGGTGTCCACATCTGC-GCACATGCCCCAGCCTCCCAAGGAAGACCTC 1038 4844 TTCATCTTGCCAGATGAGTATAAGTCTTGCTTACGGCATAAGGCGCTCTCTGAGGTCC 4903 CATAGAAATGAAGAACTGAACGTGGAGACCTTGGTGGTGGTCGACGAAAAAGATGATGCAA 1158 4904 CATAGAAATGAAGAACTGAACGTGGAGACCTTGGTGGTGGTCGACAAAAGATGATGCAA 4963 1159 AACCATGGCCATGAAAATATCACCACCTACGTGCTCACGATACTCAACATGGTATCTGCT 1218 5024 ITATITCAAAGAIGGAACAATAGGAGGAAACAITCAACAIIGCAAIIGIAGGICIGAITICII 5083 5084 CTAGAAGATGAACAGCCAGGACTGGTGATAAGTCACCACGCAGACCACACCTTAAGTAGC 5143 ------TGGATTGATGGGGAAAGATGGGGACTCGTCATGACCACGCCATC 1272 4520 TCCTCA-------------------GTGGCCCTTTCAACCTGCCAAGGCTTGTCA 4555 4616 TĠGAAACTCGGCAGAGCTGCCCAAGGCAGCTCGCCATCCCACGTACTGTACAAGAGATCC 4675 4676 ACAGAGCCCCATGCTCCTGGGGCCAGTGAGGTCCTGGTGACCTC------AAGG 4723 4724 ACATGGGAGCTGGCACATCAACCCCTGCACAGCAGCGACCTTCGCCTGGGACTGCCACAA 4783 TTACTGACTGGTCTGGATATATGTTCCTGGAAGAATGAGCCCTGTGACACTTTGGGATTT 1332 5264 GCACCCATAAGTGGAATGTGTAGTAAATATCGCAGCTGCACGATTAATGAAGATACAGGT 5323 CTTGGACTGGCCTTCACCATTGCCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT 1452 1280 CATGAAATCATGCACCATCAGCGGGGGAAAAAGAGCAGTGGCCGTGTCCGAGGTTGAGTCT 4339 562 ACCCTAGTGGCTCCTGGCTTTATTGTGCAGCGTTGGGAAAGACAGGCACTAAGTCTGTG 621 682 TCGCCATCGCATGGAGGGAAGTTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAAC 741 742 AGTCAGAAATGTCCCCGGGACAGTGTTGACTTCCGTGCTGCTCAGTGTGCCGAGCACAAC 801 802 AGCAGACGATTCAGAGGGCGGCACTACAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG 859 860 ACTTATGCAAACTCTACTGTATCGCAGAAGGATTTGATTTCTTCTTTTCTTTGTCAATA 919 920 AAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGTATAGATGGGATAT 979 622 CAGACTITACCGCCAGAGGACTICIGITICIATCAAGGCTCTTTGCGATCACACAGAAAC 4784 AAGCAGCATTTCTGTGGAAGACGCAAGAAATACATGCCCCCAGCCTCCCAAGGAAGACCTC TTCATCTTGCCAGATGAGTATAAGTCTTGCTTACGGCATAAGCGCTCTCTTCTGAGGTCC 4964 AACCAIGGCCAIGAAAAIATCACCACCTACGIGCTCACGATACTCAACAIGGTAICTGCT 1230 5204 TTACTGACTGGTCTGGATATATGTTCCTGGAAGAATGAGCCCTGTGACACTTTGGGATTT 502 CITCACCITCGGCTGAAAGGCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGC GCACCCATAAGTGGAATGTGTAGTAAATATCGCAGCTGCACGATTAATGAAGATACAGGT 1039 1099 1219 1273 1393 1230

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593 CCCGAGAACTINAICGCTACTGGACCAACGAACGAGACACTGATTGTGGAGCTGCTGTTT 2652
                                                                                                                                                                                  324 CCCGAGAACTTAATCGCTACTGGACCAACCAACGAGACACTGATTGTGGAGCTGCTGTTT 6583
                                                                                                                                                                                                                                                  653 CAGGGAAGGAACCCGGGTGTTGCCTGGGAATACTCCATGCCTTGGCTTGGGGACCGAGAAG 2712
                                                                                                                                                                                                                                                                                                                                                                        713 CAGCCCCCTGCCCAGCCCAGCTACACTTGGCCCATCGTGCGCTCTGAGTGCTCCGTGTCC 2772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADANTS; cytostatic; antidiabetic; antirheumatic; cyclic; tribritic; antidicer; vulnerary; neovascularisation; angiona; attoriates antidicer; vulnerary; neovascularisation; angiona; tet comencopathy; chronic rheumaticid arthritis; gene therapy; cyclory skin ulucer; gastric uleer; post-operative healing failure; lyssin-type ZN-metalloprocease domain; disintegrin-like domain; TSP; bhospondin type 1 domain; sexual cycle; tumour; 5P-syndrome deletion; mosme 5pl5.2.15.3; Ciri du-chat syndrome; circular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             id pFastBac1-MS/HT-PJ01256-2.
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poson In7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 773 TGCGGAGGGG 2783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 TGCGGAGGGG 6714
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5874 ACCCATGGCCACTGGACTGGACTGTCTTGGTCCCCATGCTCCAGGACTGCGGAGG 5933
                                                                                                                                                 GGAGTATCTCATAGGAGTCGCCTCTGCACCAACCCCAAGCCATCGCATGGAGGAAGTTC 1992
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                                       1813 CATGACATGTGCCGGGGAGGACAGTGTGTGAAATATGGTGATGAAGGCCCCAAGGCCC
                                                                                            1873 ACCCATGGCCACTGGTGGGACTGGTCTTCTTGGTCCCCATGCTCCAGGACCTGCGGAGGG 1932
                                                        5814 CATGACATGTGGTGCCCGGGGAGGACAGTGTGTGAAAAATATGGTGAAGAGGCCCCAAGCCC
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The invention comprises the amino acid and coding sequence of the human MDTS9 procease. The MDTS9 DNA and protein sequences of the invention are useful for screening for transforming growth factor (TGF)-bera inhibitors and for the treatment of chronic renal failure. The present DNA sequence encodes the human MDTS9 protease of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 GCAGGCCCGGCGCCATGGGACCCGCAGGGCCCTGGGAGCCCGGAGCGTCC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease MDTS9 and encoded polynuclectide, applicable in diagnosis an
screening TGF-beta inhibitors for treatment of chronic renal failure
                                                                                                                                  Human, gene; ds; MDTS9 protease; TGF-beta inhibitor; transforming growth factor-beta inhibitor; chronic renal failure.
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                                                                                                                                                                                                                                                                             /product= "Human MDTS9 protease"
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                                                                                                      Human MDTS9 protease coding sequence.
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AAL43654 standard; DNA; 3675 BP
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                2473 CCCGAGAACTTAAITGCTACTGGACCAACCAACAGACACTGATTGTGGAGCTGCTGTTT 2532
                                                  2653 CAGGGAAGGCACCCGGGTGTTGCCTGGGAATACTCCATGCCTCGCTTGGGGACCGAGAAG 2712
                                                                            2533 CAGGGAAGGAACCCGGGTGTTGCCTGGGAATACTCCATGCCTCGCTTGGGGACCGAGAAG 2592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a new isolated nucleic acid comprising a sequence that encodes a fully defined protein sequence comprising of or 1244 anima acids out that hybridises under stringent conditions with the 3575-bp sequence or its complement. The nucleic acid is useful for the preparation of a medicament for diagnosting preventing or treating disorders (e.g. using gene therapy) or diseases associated with the novel human proteins, e.g., obesity. This sequence encodes a novel human protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
64.8%; Score 1874.6; DB 25; Length 3675;
Best Local Similarity 94.4%; Pered. No.0;
Macches 2287; Conservative 0; Mismacches 179; Indels 245; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding novel human protein (NHP), useful for the preparation of a medicament for diagnosing, preventing or treating disorders or diseases associated with the NHP, e.g., obesity ,
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                                                                                                                                                                                                                                                                                                                         Novel human protease coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LEXI-) LEXICON GENETICS INC.
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                                                                                                  262 GOGTCCTCCTCCACCGGCGGAGCGGCCGGGCTGGAAAAGGGCGGGACATGGATGAA 321
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preparation of a medicament for diagnosing, preventing or treating disorders or diseases associated with the NHP, e.g., obesity

Disclosure, Column 25-30; 17pp; English.

The invention describes a new isolated nucleic acid comprising a sequence that encodes a fully defined protein sequence comprising 91 or 1224 amino acids or that hybridises under stringent conditions with the 3675-bp sequence or its complement. The nucleic acid is useful for the preparation of a medicament for diagnosing, preventing or treating disorders (e.g. using gane therapy) or diseases associated with the novel human proteins, e.g., obesity. This sequence encodes a novel human protease.

Sequence 4042 BP, 947 A; 1117 C; 1130 G; 848 T; 0 other;

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9 980 GTGAGCTCAGTGTGTGTCCACATCTGC-GCACATGCCCCAGCCTCCCAAGGAAGACCTC 1038 446 506 507 CAGACTITACOGCCAGAGACTICTGTTTCTATCAAGGCTCTTTGCGATCACACAGAAAC 566 920 AAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGTATAGATGGGATAT 979 441 326 501 561 681 802 AGCAGACGATTCAGAGGCGGCACTACAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG 859 663 TGGAAACTCGGCAGAGCTGCCCAAGGCAGCTCGCCATCCCACGTACTGTACAAGAGATCC 722 723 ACAGAGCCCCATGCTCCTGGGCCCAGTGAGGTCCTGGTGACCTC...----AAGG 770 771 ACAMGGGAGCHGGCACATCAACCCCTGCAGGGACCTTCGCCTGGGACTGCCACAA 830 GCGTCCTCCTCCTCCACCCGCGGGCCGGGCTGGAAAAGGGCGGGACATGGATGAA 321 227 degrecrecrecrecedededededededededendahadadede----- 273 32 GCTGGAAACCATCGTTCTCAGCAAACTAACACAGGAACAGAAAACCAAACACTGCATGTT 381 327 CAIGAAATCATGCACCATCAGCGGCGGAGAGAGCAGTGGCCGTGTCCGAGGTTGAGTCT 386 AGCCTAGTGGCTCCTGGCTTTATTGTGCAGACGTTGGGAAAGACAGGCACTAAGTCTGTG 621 TCGCCATCGCATGGAGGAAGTTCTGTGAGGGCTCCACTGGCACTCTGAAGCTCTGCAAC 741 742 AGTCAGAAATGTCCCCGGGACAGTGTTGACTTCCGTGCTGCTCAGTGTGCCCGAGCACAAC 801 274 -----AATATGACCTGGTCTCTGCCTACGAGGTTGACCAGGGGGATTACGTGTCC 447 ACCCTAGTGGCCTCCTGGCTTTATTGTGCAGACGTTGGGAAAGACAGGCACTAAGTCTGTG 382 CTCACTCAATATGACCTGGTCTCTGCCTACGAGGTTGACCACAGGGGGGATTACGTGTCC CATGAAATCATGCACCATCAGCGGCGGAGAAGAGCAGTGGCCGTGTCCGAGGTTGAGTCT 502 CTTCACCTTCGGCTGAAAGGCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGC 387 cricaccricecorgaagerccaeecaeeacriceaegeserricae CAGACTTTACCGCCAGAGGACTTCTGTTTCTATCAAGGCTCTTTGCGATCACAGAAAC Pred. No. 0; 0; Mismatches 179; Indels 245; Gaps 64.8%; Score 1874.6; DB 25; Length 4042; 84.48; Matches 2287; Conservative Best Local Similarity 567 rccrcA--442 295 289 262 622

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1039	TTCATCTTGCCAGATGAGTATAAGTCTTGCTTACGGCATAAGGGCTCTCTTCTGAGGTCC 1
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m	GCACCCATAAGTGGAATGTGTAGTAAATATCGCAGCTGCACGATTAATGAAGATACAGGT 139
1311	GCACCCATAAGTGGAATGTGTAGTAAATATCGCAGGTGCACGATTAATGAAGATACAGGT 137
	CTIGGACTICACCATTGCCCATGAGTCTGGACACAACACTTTGGCATGATTCATGAT 14
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1453	GGAGARAGGARATGTGTRARARGTCCGAGGGCRACATCATGTCCCCTRCATTGGCAGGA 151
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່ຕໍ	GAGAAATTGCCAGGAGAATTATATGATGCAAACACACAGGGGAAGTGGCAGTTCGGAGAGAG 169
	AAAGCCAAGCICIGCAIGCIGGACIITAAAAAGACACAICIGIAAAGCCCIGIGGCAI 17
1671	~
1753	CGIATTGGAAGGAAATGTGAGACTAAATTTATGCCAGCAGAGAGGCACAATTTGTGGG 1812
1731	
1813	CATGACATGAGGAGGGGGGGGAGGAGGGGAATATGGAGATGAAGGCCCCAAGCCC 1872
1791	
1873	173 ACCATGGCCACTGGTCGGACTGGTCTTCTTGGTCCCCATGCTCCAGGACCTGCGGAGGG 1932
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GGAGTATCTCATAGGAGICGCCTCTGCACCAACCCCAAGCCATCGCATGGAGGAAGITC 1970
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                                                    GTTGACTTCCGTGCTGCTCAGTGTGCCGAGCACAACAGCAGACGATTCAGAGGCGGCAC
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                                                                                         TACAAGTGGAAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATC
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                TGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAATGTCCCCGGGACAGT
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Autoimmune disease; allergy; addiction; asthma; transplantation; watter versus host disease; systemic lupus erythematosus; soleroderma; grate versus host disease; HIV infection; human immunodeficiency virus; psoriasis; Crchm's disease; HIV infection; human immunodeficiency virus; atherosclerosis; cirrhosis; rheumatoid arthritis; diabetes; pancratitis; thromboyvopenia; bleeding disorder; metabolic disorder; obesity; my plucose transport defect; glomerulonephritis; hypercalcaemia; polystic kidney disease; renal tubular acideois; skin disorder; hoperial disorder; humarel disorder; pont disorder; muscle disorder; muscle disorder; muscle disorder; muscle disorder; muscle disorder; infection; muscle disorder; minary system disorder; respondation disorder; hyperality disease; dental infection; sprewth disorder; reproductive disorder; hyperality disorder; viral infection; bacterial infection; manapognadiam; fertility disorder; viral infection; disorder; sphanapognadiam; manapognadiam; m 2000US-241040P. 2000US-241058P. 2000US-241063P. 2000US-241243P. 2000US-242152P. 2000US-242482P. 2000US-259028F. 2001US-269813F. 2001US-286324F. 2001US-294108F. 2000US-242612P. 2000US-242880P. 2000US-242611P. 2000US-242881P. 2001US-303698P. 17-OCT-2001; 2001WO-US32496. (CURA-) CURAGEN CORP. WO200233087-A2. 17-0CT-2000; 23-0CT-2000; 23-0CT-2000; 23-0CT-2000; 24-0CT-2000; 24-0CT-2000; 29-DEC-2000; 20-PEB-2001; 25-APR-2001; 29-MAY-2001; Homo sapiens. 17-OCT-2000; 09-JUL-2001; 16-OCT-2001; 25-APR-2002 Edinger S, Willet I,

Gerlach V, MacDougall JR, Malyankar UM, Smithson G; Peyman JA, Stone DJ, Gunther E, Bilserman K, Shimkets RA; Guo X, Patturajan M, Taupier RJ, Burgess CE; D, Kekuda R, Spyrek KA, Gangolli EA, Fernandes ER; Padigaru M, Zerhusen BD, Gorman L;

WPI; 2002-590434/63. P-PSDB; ABG76895

and cytoplasmic, muclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheiner's disease, cardiomyopathy, metabolic disease diabetes

Claim 8; Page 14-15; 305pp; English.

The present invention relates to new NOVX (NOV1-10) polypeptides. The molecules of the invention are useful for treating or preventing a NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, or a disorder related to cell signal processing and metabolic pathway modulation in humans. NOVX polypeptides, nucleic acides and antibodies are useful for treating or preventing disorders or syndromes including breast cancer, Alzheimer's disease, epilepsy, Huntington's disease, anxiety, behavioural disorders, multiple sclerosis, mysthemia gravis, neurodegeneration, Parkinson's disease, pain, stroke, aucoimmune disease, allergies, addiction, athma, endometriosis, graft versus host disease, systemic lupus exythemacousus, scleroderma, transplantation, psoriasis, Crohn's disease, HIV (human immunodeficiency virus) infection,

Human; NOVX; cardiomyopathy; atherosclerosis; cell signal processing; breast cancer; Alzheimer's disease; epileppy; Huntington's disease; anxiety; behavioural disorder; multiple sclerosis; myasthenia gravis; neurodegeneration; Parkinson's disease; pain; stroke; endometriosis.

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atherosclerosis, cirrhosis, rheumatoid arthritis, diabetes, thromboveropenia, bleeding disorders, metabolic disorders, obesity, glucose transport defect, glomerulonephritis, hypercalcaemia, polycystic glucose transport defect, glomerulonephritis, metabolicis, skin disorders, chidney disease, pandreatitis, renal tubular acidosis, skin disorders, congenital disarchosa, respiratory disease, gastro-intestinal diseases, muscle, bone, joint and skeletal disorders, haematopoietic disorders, usinals, some disorders, secoporosis, dental disease and infection, growth and reproductive disorders, hypogonadism, fertility, and/or other pathologies and disorders, viral, bacterial, or parasitic infections. The present nucleic acid sequence encodes a NOVX protein of the invention.	Similarity 81.9%; Pred. No. 0; 4, Conservative 0; Mismatches 34; Indele 490; Gaps 8;	CGCTCCTGGATGAAGCCCGGGGGGGGGGGGGGGGGGGGG	TTGGCGCAGGTGGCCGAGGTGAGGTCCCGGGCGCTCCCACCAGCGGGAACCGCGGG 120	TCCGGACACTGGACGCGAGTCCCCCCGGGGCTCCTCTCCCGGCGACCCCGCCGTCTCACC 180	GCGATGTCGCCGCTGTTTTCCGCAGGCACCTGCGTGCGCCATGGGACCGGCAGCGCAGC 240	GCCTGGGAGCCCGAGCGTCCCCGCGCGCGGAGCGGCCGGGCTGGATGGA	AAAGGGCGGGACATGGATGAAGCTGGAAACCATCGTTCTCAGCAAACTAACACAGGAACA 360	GARARCCARACATOCATGATCTCACTC ANTATGACCTGGTCTCTGCCTRCGAGGTT 417	GACCACAGGGGCGATTACGTGTCCCATGAAATCATGCACCATCAGGGGCGGAGAAGAGA 477	GTGGCCGTGTCCGAGGTTGAGTTCTCTTCACCTTCGGCTGAAAGGCCCCAGGCACGACTTC 537	CACATGGATCTGAGGACTTCCAGCAGCCTAGTGGCTCTGGCTTTATTGTGCAGACGTTG 597	9 GGAAAGACAGGCACTAAGICTGTGCAGACTTTACCGCCAGAGACTTCTGTTTCTATCAA 657 	9 GGCTCTTTGCGATCACACAGAAACTCGCCATGGCATGGGGGAAGTTCTGTGAGGGCTCC 717 	ACTOGCACTCTGAAGCTCTGGAACAGTCAGAAATGTCCCCGGGACAGTGTTGACTTCCGT 777	GCTGCTCAGTGTGCCGAGCACAACAGCAGACGATCAGAGGGGGGCACTACAAGTGGAAG 837
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898	TICTICITICITITCITICICAAAIAAAGICAAAGAIGGGACICCAIGCICGGAGGAIAGCCGI 957
958	ARTOTTTGTATRGATGGGATATGTGAGCTCAGTGTGGTGTCCACATCTGCGCACATGCCC 1017
1018	CAGCOTCCCAAGGAAGACCTCTTCATCTTGCCAGATGAGTATAGAGTCTTGCTTACGGGT 1077
1078	AAGGGCTCTCTTCTGAGGTCCCATAGAAATGAAGAACTGAACGTGGAGACCTTGGTGGTG 1137
1138	GTCGACAAAAAGHTGANGCAAAACATGGCCATGAAAATATCACCACCTACGTGCTCACG 1197
1198	Alacticaacanggtaictigettitatticaaagatogattigatigagaaagatgggactigt 1257
1258	CATGACCACGCCATCTTACTGACTGGTCTGGATATATGTTCCTGGAAGAATGAGCCCTGT 1317
1239	1238
1318	GACACTTTGGGATTTGCACCCATAAGTGGAAATGTGGTAGTAAATATGGCAGCTGCACGATT 1377 GACACTTTGGGATTTGCACCCATAAGTGGAATGTGTGCAATTGTTGCAATT
1378	AATGAAGATACAGGTCT19GACT1GGCCTTCACCATTGCCCATGAGTCTGGACACAACTTT 1437
1263	AGGTCTGATTC
1438	GGCATCATTCATGGAGAAGGAACATGTTAAAAAGTCCGAGGGCAACATCATGTCC 1497
1498	CCIACATIGGCAGGACGCAAIGGAGICITCICCIGGICACCCIGCAGCCGCCAGIAICIA 1557
1274	1273
1558	GACAAATTTCTAAGGACGGCTCAAGCTATCTGCCTTGCTGATCAGCCAAAGCCTGTGAAG 1617
1274	1273
1618	GAATACAAGTATCCTGAGAAATTGCCAGGAGAATTATATGATGCAAACACACAGTGCAAG 1677
1274	1273
1678	HOSCAGITCGGAGAGAAGCCAAGCTCTGCATGCTGGACTITAAAAGGACATCTGTAAA 1737
1274	
1738	GCCCTGGGGCCRTCGTTGGAAGGAAATGGAACTAATTTATGCGAGCGAAA 1797 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
1798	GGCACAATTYGTGGGCATGACATGTGGTGGCGGGGAGGACGAGTGTGAAATATGGTGAT 1857
1858	GAAGGCCCAAGCCCAAGGCCACAGGCGGACTGGTCTTCTTGGTCCCCATGCTCC 191

Human ADAM-TS 7-like gene #1.

(first entry)

05-NOV-2002

ABS59325;

When the content of t Gerlach V, MacDougall JR, Malyankar UM, Smithson G; Peyman JA, Skone DJ, Gunther B, Bilerman K, Shimkets RA; Guo X, Patturajan M, Taupier R, Burgess CE; D, Kekuda R, Spytek KA, Gangolli EA, Fernandes ER; Human; NOVX; cardiomyopathy; atherosclerosis; cell signal processing; 200005-241058P 2000005-241243P 2000005-2412482P 2000005-242182P 2000005-242182P 2000005-242611P 2000005-242612P 2000005-242612P 2000005-242612P 2000005-242612P 2000005-242612P 2000005-242612P 2000005-242612P 2000005-24108P 2000105-26913P 2000105-26913P 2000105-26913P 2000105-26913P 2000105-26913P 17-OCT-2001; 2001WO-US32496 (CURA-) CURAGEN CORP. WPI; 2002-590434/63. P-PSDB; ABG76896. WO200233087-A2 117-0CT-2000; 2 17-0CT-2000; 2 20-0CT-2000; 2 23-0CT-2000; 2 23-0CT-2000; 2 24-0CT-2000; 2 24-0CT-2000; 2 24-0CT-2000; 2 25-DEC-2000; 2 29-DEC-2000; 2 Padigaru M, Zerhusen BD, Homo sapiens. 17-OCT-2000; 29-MAY-2001; 25-APR-2001; 09-JUL-2001; 16-OCT-2001; 25-APR-2002 Edinger S, Gorman L;

and

Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheimer's disease, cardiomyopathy, metabolic disease diabetes -

The

The present invention relates to new NOVX (NOV1-10) polypeptides. T molecules of the invention are useful for treating or preventing a

Claim 8; Page 17; 305pp; English.

BP

ABS59325 standard; DNA; 2902

RESULT 11 ABS59325 ID ABS

C disorder related to cell signal processing and metabolic pathway modulation in humans. Now polypeptides, muslet acids and antibodies are useful for treating or preventing disorders or syndromes including breast cancer. Alzheimer's disease, pallepsy, Huntington's disease, anxiety, behavioural disorders, multiple scierosis, mystehenia gravis, neurodegeneration, Parkinson's disease, pain, stroke, autoimmus edisease, allergies, addiction, asthma, endometriosis, graft versus host disease, systemic lupus erythematosus, scleroderma, transplantation, psoriasis, Crohn's disease, HIV (human immunodeficiency virus) infection, atthosomorytopenia, bleeding disorders, metabolic disorders, obsity, glucose transport defect, glomerulomephitis, hypercalcemmia, polycystic kidney disease, pancreatitis, renal tubular acidosis, skin disorders, congenital diarrhoea, respiratory disease, gastro-intestinal diseases, culthary system disorders, using disorders, hamenapole tell disorders, culthary system disorders, viral, dental disease and infection, growth and reproducts, hypothemic disorders, culthary system disorders, viral, bacterial, or parasitic infections. The present mucleic acid sequence encodes a NOVX protein of the such as cardiomyopathy, atherosclerosis, or NOVX-associated disorder,

Sequence 2902 BP; 699 A; 752 C; 777 G; 674 T; 0 other;

159 CACCAGCGCGGAAACCGCGGGTCCGGACAGCTGGAGGCGAGTCCCCCGCGGGTCCTCTCC 120 219 279 280 GGAGCGGCCGGGCTGGATGGAAAAGGGCGGGACATGGATGAAGCTGGAAACCATCGTTCT 339 399 241 459 301 CAGCGGCGGAGAAGAGCAGTGGCCGTGTCCGAGGTTGAGTCTCTTCACCTTCGGCTGAAA 519 416 639 cesserrirreaacerriccaarerreserreseresassaacaseareserresassa 476 GACTICIGITICIATCAAGGCICITIGCGAICACACAGAAACTCGCCATCGCATGGAGGG 699 GAATAATAACAAATGCAA-----TGCTTGGAGAATCGGCCCTGGCTTCAACCAGAAAG 529 700 AAGTTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAATGTCCCCGG 759 99 TIGGCGGCGCTGTGGAIGCTGTTGGCGCAGGTGGCCGAGCAGGTGAGTCCGGGCGCTCC GTCTCTGCCTACGAGGTTGACCACAGGGGGATTACGTGTCCCATGAAATCATGCACCAT CACCAGCGCGGAAACCGCGGGTCCGGACAGCTGGAGGCGAGTCCCCCCGCGGCTCCTCTCC CATGGGACCCGCAGCGCCAGGGCTCCGGAGCGTCCTCCTCCTCCACCCGC GTCTCTGCCTACGAGGTTGACCACAGGGGGGGATTACGTGTCCCATGAAATCATGCACCAT Adagcchigagagcrchagacr----ererereshageccrrrccarrecrarrerese 580 ITTATIGICCAGACGIIGGGAAAGACAGGCACTAAGICTGIGCAGACIITACCGCCAGAG GGCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGCAGCCTAGTGGCTCCTGGC Score 1695; DB 24; Length 2902; Pred. No. 0; 0; Mismatches 315; Indels 339; Gaps Query Match Best Local Similarity 78.1%; Matches 2333; Conservative 61 220 40 001 160 121 181 236 400 242 460 302 520 362 640 477 ò ద g à 8 g q 8 8 g ð ò g à ò ò 셤 8 ద ઠે ò

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qq	590 GAGGCAGATTACTTACGCACTTCCTTCACACCTCTCATGGAAACTCGGCAGAGCT 649
ò	820 CGGCACTACAAGGCTTACACTCAAGAAGCCGACTTATGCAAACTCTACT 877
đ	650 gcccaaggcaactcccatcccacaractacaagaagagagaccccgaagactctcaagg 709
ò	878 GIAICGCAGAAGGATITGAITICITTCTTTTCTCAAAAAAAGICAAAGAGGGACTC 937
QQ	710 ACATGGGAGCTOGCACATCAACCCCTGCACACCAGCAGCA 747
à	938 CATGCTCGGAGGAFAGCCGTAATGTTTGFATAGATGGGATATGTGAGCTCAGTGTGTGT 997
qq	748 CCTTCGCCTGGGACTGCCACAAAGCAGCATTCTGTGGAAGACGCAAGAAAT 800
λ	998 CCACATCTGCGCACATGCCCCAGCCTCCCAAGGAAGACCTCTTCATCTTGCCAGATGAGT 1057
QQ	801ACATGCCCCAGCCTCCCAAGGAAGACCTCTTCATCTTGCCAGATGAGT 848
ò	1058 ATAAGTCTTACCTACGGCATAAGCGCTCTCTTCTGAGGTCCCATAGAATGAAGAACTGA 1117
qa	849 ATAAGTCTTGCTTACGGCATAAGCGCTCTCTCTGAGGTCCCCATAGAAATGAAGAACTGA 908
ò	1118 ACCTGGAGACCTTGGTGGTCGACAAAAAGATGATGCAAAACATGGCATGAAATA 1177
qq	909 ACGTGGAGACCTTGGTGGTGGTCGACAAAAGATGATGCAAAACCATGGCCATGAAATA 968
ò	1178 TCACCACCTACGTGCTCACGATACTCAACATGGTATCTGCTTTATTCAAAGA 1229
qq	CACCTACGTCCTCACGATACT
à	1230 1229
q	1029 TAGGAGGAAACATCAACATTGCAATTGTAGGTCTGATTCTTCTAGAAGATGAACACCCAG 1088
ò	1230
qu	1089 GACTGGTGATAAGTCACCACGCAGACCACACTTAAGTAGTTTCTGCCAGTGGCAGTCTG 1148
ò	1232 GATTGATGGGAAAGATGGGACTCGTCATGACCACGCCATCTTACTGACTG
qc	1149 GATTGATGGGGAAAGGACTGTCGTCATGACCACGCCATCTTACTGACTG
ö	1292 TATGITCCTGGAAGAAJGAGCCCTGTGACACTTTGGCACTTTGCACCCATAAGTGGGAATGT 1351
qq	1209 TATGTTCCTGGAAGAATGAGCCCTGTGACACTTTGGGATTTGCACCCATAAGTGGAATGT 1268
à	1352 GTAGTAAATATCGCAGCTGCACGATTAATGAAGATACAGGTCTTGGACTGGCCTTCACCA 1411
qq	1269 GTAGTAAATATCGCAGCTGCACGATTAATGAGATACAGGTCTTGGACTGGCCTTCACCA 1328
ò	2 TIGCCCATGAGTCTGGACACAACTTTGGCATGATTCATGATGGAGAAGGGAACATGTC
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ò	1472 AAAAGTCCGAGGCAACATCATGTCCCCTACATTGGCAGGACGCAATGGAGTCTTCTCCT 1531
අු	1389 AAAGTCCGAGGGCAACATCATGTCCCCTACATTGGCAGGACGCAATGGAGTCTTCTCCT 1448
λ	1532 GGTCACCCTGCAGCGCCGCAGTATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCC 1591
qq	1449 GGTCACCCTGCAGCGCCAGAATTCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCC 1508
ò	1592 INGCIGATCAGCCAAAGCCTGTGAAGAATACAAGTAICCTGAGAAATTGCCGGGAGAAT 1651
qq	1509 TTGCTGATCAGCCAAAGCCTGTGAAAGAAAACAAGTATCCTGAGAAATTGCCAGGAGAAT 1568
δλ	1652 TATATGAACACACACAGTGCAAGTGGCAGTTGGGAAAAGCCAAGCTCTGCATGC 1711

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Claim 5; Page 158-159; 168pp; English.
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                                                                                                                                                                                                                        cDNA encoding human protease PRTS4.
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                                                                                                                                              ABK86137 standard; cDNA; 4888
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16-NOV-2000; 2000US-249826P.
20-NOV-2000; 2000US-252303P.
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                                                                                                                                                                                           /*tag= a
/product= "PRTS4 protein"
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antagonist are useful for treating a disease or condition associated
The PRTS protein is also useful as an immunogen for preparing polyclonal
CC or monoclonal antibodies by hybridoma technology. An antibody that binds
the PRTS proteins is useful for detection and purification of the
pRTS proteins and can be used to diagnose a condition or disease associated
the PRTS proteins is useful for detection and purification of the
proteins and can be used to diagnose a condition or disease associated
the proteins and can be used to diagnose a condition or disease associated
the proteins of pastroin are useful for in a biological smalle. The
sequences of the invention are useful for diagnosis, treatment and
CC prevention of gastrointestinal disorders such as qastrifis, ulcerative
colitis, Reye's syndrome, etc. cardiovascular such as atherosclerosis,
disorders such as acquired infarction, etc. autoimmune/inflammatory
disorders such as acquired infarction, etc. autoimmune/inflammatory
disorders such as acquired infarction, etc. autoimmune/inflammatory
cave a disease, etc. pell proliferative disorders such as
cushing's syndrome, epithelial disorders such as dermatitis, scabies,
cersem, etc. neurological disorders such as dermatitis, and isease,
dementia, Alzheimer's disease, Huntington's disease, multiple sclerosis,
cerson, etc. or neurological disorders such as pervoductive disease,
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λö	1604	CAAAGCCIGIGAAGGAATACAAGTATCCIGAGAAATIGCCAGGAGAATTATATGATGCAA 1663
ପ୍ର	23	AGGAATACAAGTATCCTGAGAAATTGCCAGGAGAATTATATGATGCAA 150
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qq	2003	ACAACAGCAGCATTCAGAGGGCGCGCACTACAGTGGAAGCCTTACACTCAAGTAGAAG 2062
È	2144	ATCAGGACTTATGGAAACTCTACTGTATGGCAGAAGGATTTGATTTCTTTGT 2203
දු	2063	ATCAGGACTTATGCAAACTCTACTGTATCGCAGAAGGATTTGATTTCTTCTTTTTTTT
ò	2204	CAAATAAAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGTATAGATG 2263
g	2123	CAAATAAAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGTATAGATG 2182
ò	2264	GGATATGTGAGAGAGTTGGATGTGACAATGTCCTTGGATCTGATGCTGTTGAAGACGTCT 2323
qα	2183	GGATATGTGAGAGGTTGGATGTGACAATGTCCTTGGATCTGATGCTGTTGAAGACGTCT 2242
ò	2324	GTGGGCTGTCTAACGGGAATAACTCAGCCTGCACGATTCACAGGGGTCTCTACACCAAGC 2383
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ò	2444	GCATCTAIGAAAIGAACGTCTCTACCTCCTACATTTCTGTGCGCAATGCCCTCAGAAGGT 2503
qq	2363	GCATCTATGAAATGAAGGTCTTACTCCTACATTTCTGTGCGCAATGCCCTCAGAAGGT 2422
ò	2504	ACTACCTGAATGGGCACTGGACCGTGGACTGGCCCGGCCGG
qq	2423	ACTACCTGAATGGGCCACTGGACCGTGGACTGGCCCGGCCGG
δλ	2564	CTTTCGACTACAGACGGTCCTATAATGAGCCCGAGAACTTAATCGCTACTGGACCAACCA
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                         The invention relates to a polypeptide belonging to the ADAMTS family is selected from sequences appearing as AAM79469, AAM79497 and AAM79499, a protein that contains the polypeptide, AAM794949 and AAM79499 by the polypeptide and the contains the polypeptide, a protein having not less than 504 homology with the amino acid sequence of the polypeptides or a polypeptide modified from any of the polypeptides but with some amino acids deleted, substituted, added or inserted. Also included are the polymented secondary is a recombinant vector containing any of the polymented as a transformant which is transformed with the recombinant vector, producing the polypeptide, protein or peptide by culturing the transformation and recognize the polypeptide, protein or peptide and screening compounds to promote or inhibit activity of the
                                                                                                                                                                                                                                                               antiarthritis antiulser, vulnerary, neovascularisation, angional diabelis cometropathy, chronic rheumatoid arthritis, gene therapy; refractory skin ulcer; gastric ulcer; post-operative healing failure; reprolysin-type ZN-metalloprocease domain; disintegrin-like domain; TSP1, thrombospondin type 1 domain; sexual cycle; tumour; SP-syndrome deletion; chromosome 5p15.2-15.3, Cri-du-chat syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
                                                                                                                                                                                                                                                     ss; gene; ADAMTS; cytostatic; antidiabetic; antirheumatic;
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                                                                        2663 CCATCGTGCGCTCTGAGTGCTCCGTGTCCTGCGGAGGGGG 2702
                                                                                                                                                                                                                             Human cDNA encoding partial ADAMTS protein #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "No start codon"
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                                                                                                                                                                                                                                                                                                                                                                                 Socation/Qualifiers
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(MITS-) MITSUBISHI PHARMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "ADAMTS"
                                                                                                                                                   ABK49821 standard; cDNA; 4234
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polypeptide or protein, or to promote or inhibit expression of the polypeptide, by using the polypeptide, protein, peptide, the polyprolecoide, vector, transformant or/and antibody, particularly in the polypeptide, protein, peptide, the carticularly in the polyprolecoide or test compound for contact before evaluating the activity by measuring signal changes. The polypeptide and encoded gene are applicable in diagnosis and screening compounds for drug compositions in reating diseases due to neovascularisation, diabetic omentopathy, chronic rheumatoid arthritis, angioma, refractory skin and gastric ulcers and post-operative healing failure, including gene therapy.

The gene encoding such polypeptide has conserved reprolyabin-type ZN metalloprotease domain, disintegrin-like domain and 19P1 (thrombospondin type 1) domain. Its encoded protein is characterised by high expression type 1) domain. Its encoded protein is characterised by high expression convaries, changes in expression dose depending on the sexual cycle, a decrease in tumour cell and location of the gene on the 5P-syndrome delection site on thromosome 5pls. 2-15.3 (associated with EV-syndrome) the invention.
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Matches 1772, Conservative
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The invention relates to a polypeptide belonging to the ADAWTS family is selected from sequences appearing as AAU7946, AAU79497 and AAU79499, and Eacted from sequences appearing as AAU7946, AAU79497 and AAU79499.

Selected from sequences appearing as AAU7946, AAU79497 and AAU79499, a protein that contains the polypoptide, a protein having not less than 504 homology with the amino acid sequence of the polypeptides or a polypeptide but with some amino acids deleted, substituted, added or inserted. Also included are the polypeptides endeding the polypeptides (or their complementary strands or variants), a recombinant vector containing any of the polymucleotides, a transformant which is transformed with the recombinant vector, proximing the polypeptide and screening compounds to promote or inhibit activity of the polypeptide or protein or to promote or inhibit activity of the polymucleotide by using the polypeptide, protein, peptide, the polymucleotide by using the polypeptide, protein, peptide, the polymucleotide, vector, transformant orfand antipolody, particularly in playmucleotide, vector, transformant orfand antipolody, particularly in the presence of a test compound for contact before evaluating the activity by measuring signal changes. The polypeptide and encoded gene
   1957 ACTCCATGCCTCGCTTGGGGACCGAGAAGCAGCCCCTGCCCAGCCCAGCTACACTTGGG 2016
                                                                                                                                                                                                                                                             ds; ADANTS; cytostatic; antidiabetic; antirheumatic; cyclic; antialritic; antiulcer; vulnerary; neovascularisation; angloma; diabetic omentopathy; chronic rheumatoid arthritis; gene therapy; refractory skin ulcer; gastric ulcer; post-operative healing failure; reprolysin-type ZN-metalloprotease domain; disinegrin-like domain; thrombospondin type I domain; sexual cycle; tumour; 5P-syndrome deletion; pRasteacl-MG/MT-P0012Sc. 15.3; CT.-du-chat syndrome; circular;
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Baculovirus.
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                                                                                                          TGCCAGCAGCAGGCACAATTTGTGGGCATGACATGTGGTGCCGGGGGAGGACAGTGTG
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are applicable in diagnosis and screening compounds for drug compositions in treating diseases due to neovaecularisation, diabetic omentopathy, chronic rheumatoid arthritis, angioma, refractory skin and gastric ulcers and post-operative healing failure, including gene therapy. The gene encoding such polypeptide has conserved reprolysin-type ZN metalloprocease domain, disintegrin-like domain and TSP1 (thrombospondin type 1) domain. Its encoded protein is characterised by high expression in oversession descrease in tumour cell and location of the gene on the Servain cried, adeletion site on chromosome 5915.2-15.3 (associated with Cri-du-chat syndrome). The present sequence is the expression Plasmid prastBaci-HT-PJ01256 used to express DNA encoding an ADAMTS protein.
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ABK90322 standard; DNA; 1668 BP

ABK90322;

21-OCT-2002 (first entry)

DNA encoding human ADAM-TS-like Zinc metalloprotease.

ADAM TS-like Zinc metalloprotease; gene; human; ds; TNF-antagonist; CDS-antagonist; COSP, congestive heart failure; mycocardial infarction; ischaemic heart disease; arrhythmia; hypertension; vascular disease; cerebrovascular disease; dementia; multiple sclerosis; strock; Alsease; motor neuron disease; dementia; multiple sclerosis; strock; Alseamer's disease; dementia; huntington's disease; Creutzfeld-Jakob disease; dementia; schizophrenia; psychosis; attention deficit disorder; chromosome 5.

Homo sapiens.

Location/Qualifiers .1668

'product= "ADAM-TS-like zinc metalloprotease" æ /*tag=

/partial /note= "No start or stop codons shown"

WO200257461-A2

25-JUL-2002

09-JAN-2002; 2002WO-EP00129.

18-JAN-2001; 2001US-262034P.

(FARB) BAYER AG

z nuz

WPI; 2002-575457/61. P-PSDB; ABG31503. New isolated polynucleotide encoding an ADAM-TS-like zinc the training, ameliar and the tree training, ameliar and or treating dystunctions such as COPD, CNS and cardiovascular disorders

Claim 1; Fig 1; 119pp; English.

This invention relates to a novel isolated polymucleotide encoding an CARM-TS-like zinc metallogrotesse polypeptide. The protean of the invention may have cardiant, asotropic, antiarrhythmic, hypotensive, autiparkinsonian, anciropic neuropic antiarrhythmic, hypotensive, antiparkinsonian, anci-HV, neuroleptic and tranquiliser activity. The DNA sequence of the Invention may be used in gene therapy as a consequence of the Invention may be used in gene therapy as a CR - antagonist or a CR - antagonist. The Invention last compitieses an expression vector containing the ADAM-TS-like zinc metalloprotease. These reagents can be used in the manufacture of a medicament for disorders such as CORD, cardiovascular disease of a medicament for disorders such as CORD, cardiovascular disease. Congestive heart failure, myocardial infarction, ischaement heart disease, atrial and ventricular arrhythmias, hypertension and peripheral exclusive heart failure, myocardial infarction, ischaement, east, according and cerebrovascular disorders (Parkinson's disease, corticobasal degeneration, motor neuron disease, dementia, multiple sclerosis, stroke, Alzhelmer's disease, Huntington's disease, contextor, Motor neuron disease, dementia, multiple sclerosis, stroke, Alzhelmer's disease, Huntington's disease, dementia, schiophrafia, psychosis and attention can deficit disorders). Pharmaceutical compositions of the invention can excluse allogrotease of the invention, this gene is located on human chromosome 5.

Sequence 1668 BP; 462 A; 392 C; 426 G; 388 T; 0 other;

47.7%; Score 1381.8; DB 24; Length 1668; 98.9%; Pred. No. 0; Query Match Best Local Similarity

1;	1289	1349	371	1409	1469	-	LC)	551	1589	1649	671	1709	1769	782	1829	1889	902	1949	CV	2009	9	1082	2129	2189	1202	4	1262	2309	N
Gaps	CTGGA	GGAAT	GGAAT	TTCAC	ATGTG	ATGTG	TTCTC	Trere	ATCTG	GGAGA	GGAGA	TGCAT	SAAATG	SAAATG	HIIII	regre	TGGTC	PAGGAG [[[[]]	raggag	ACTCG 	GCTGC	GCTGC	CCTTA 	GATTT	GATTT	CGTAA	CGTAA	GATGC	CALGC
6	ACTGGT	ATAAGI	ATAAGI	11100CC	GGGAAC	GGGAAC	GGAGTC	GGAGTC	CAAGC	TTGCCZ	TIGGG	AAGCTC	GGAAG	GGAAGG	CATGTG	rggcca	GGCCAC	ATCTCA1	ATCTCA	200100 	TTCCG	TTCCG	TGGAAC TGGAAC	GGATTI	GGATT	SGATAGO	GATAG	CGATC	GGGRIC
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7; II	CCACGCCATCTTACTGACTGGTCTGG	SGGATT	3GGATT	TACAGG	TCATGA	rcatga.	36CAGG	Séchée	TCTAAG [TCTAAG	STATCC	GTATCC	CGGAGA CGGAGA	GTGCCA	Grecca	TTGTGG	CAAGCC	CAAGCC	CGGAGG	CGGAGG	GAAGTT	GGACAG	GGACAG	GCGGCA GCGGCA	CTGTAT	CTGTAL	TCCATG	TCCATG	TGACAA	I'GHCAM
ches	TGACCA 	CACTIT	CACTTT	TGAAGA	CATGAT	CATGAT	TACATT	TACATT	CAAATT	ATACAA	ATACAA	GCAGTT CAGTT	CCTGTG	CCTGTG	CACAAT	AGGCCC	 AGGCCC	GACCTG	GACCIG	TGGAGG	11111	ಸಾಂಭಾರ	CAGAGG - CAGAGG	ACTCTA	ACTCTA	TGGGAC	TGGGAC	TGGATG	2.WOOL
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ν.	TGGGAC	TGAGCC	TGAGCC	SCTGC&C	BACACAA	SACACAA	ACATCAT	CATCAT	SCCAGTA SCCAGTA	ACCTGI	AGCCTGT	CACAGTO	ACATCTG		CAGCAGO	AATATGO	ATATGO	CCCATC	CCCCATC	CAAGC	ACAGTCA	ACAGTCA	ACAGCAC 	AGGACTI	GGACT	ATAAAG:	TAAAGI	PATGTGP	CATGLO
tive	SGAAAGA SGAAAGA	SGAAGAA	SGAAGAZ	ATCGCAC	AGTCTGC	AGTCTG	AGGGCN	AGGGCA.	SCAGCC 1	AGCCAA4	AGCCAA	CAPACAC	AAAAGG	AAAAGG	TANTGCC	STGTGA	 GTGTGA	CTTGGT	CTTGGT(CCAACC CCAACC	TCTGCA	ICIGCA	AGCACA AGCACA	AAGATC	AAGATC	TGTCAA	TGTCAA	ATGGGA,	ATGGGA
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5; Con	TCGAT	TATAT	TATAL	GTGTA	CATTG	CATTG	TAAAA	CAAAA	CTGGT CTGGT	CCTTG	CCTTG	ATTAT ATTAT	GCTGG	GCTGG	TGAGA	GGGAG	- - - - - - - -	GGACT	GGACT	70000 	CACTC	CACTO	TCAGT CAGT	0-	CACTO	CTTCT	130	TGTTT	Tern
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Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Ruh on: October 28, 2003, 18:20:48; Search time 5371 Seconds Title: Parfect score: 2855-281-151A-7 Sequence: 108:09-981-151A-7 Sequence: 108:09-981-151A-7 Sequence: 108:09-981-151A-7 Sequence: 108:09-981-151A-7 Sequence: 22851392 seqs, 12152238056 residues Total number of hits satisfying chosen parameters: 45562784 Minimum DB seq langth: 0 Maximum Match 0% Maximum Match 0% Maximum Match 0% Maximum Match 100% Lising first 45 summaries Database: EST: Sem esthar* Si em esthar* Si em esthar* Si em estro:* Si em estr		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES SUMMARIES

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/strain="C57Bi,6J"

/db_xref="FaNTOM_DB:6330405121"

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                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Maiyama,J., Nishi,Y., Kitsunai,T., Tasahico,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Sumi,N., Ishi,K., Matsumoco,H., Sakaguchi,S., Iksahineqi,Y., Harada,A., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Chara,E., Watshiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Chara,E., Watshika,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Sequencing pipeline with 38 multicashis system-184-format connon Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-langth cDNAs
Nature 420, 563-573 (2002)
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Please visit our web site for further details.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-langth CDMAs
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKBN), Laborascry for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC). RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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	Qy 27: Db 310	2735 ACACTTOGGCCATCGTGCGCTCTGGAGTGCTCCTGCGCGAGGGGT 2784 	
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	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AKO36137. GI:26085046 HTC; CAP trapper. HTC; CAP trapper. Mus musculus (house mouse) Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus musculus Mus	
GAGACH 2321 CACTCTGA 2017 	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	Tanking and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349638	
	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	2. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of Cap-trapper-selected cDMss to Normalization and subtraction of Cap-trapper full-1-nght cDMs, libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
CTTCTTT 2197 TTTCTTG 2561 TGTTGTA 2257 CGTCTGCA 2621	REFERENCE AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komo,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishihi,Y., Nakamura,S., Hazama,M., Nishihe,T., Hazada,A., Yamamoto,R., Matsunco,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matahiki,M., Yonday,Y., Itahikawa,T., Matsuura,S., Kawai,J., Okazaki,Y., Murametsu,M., Tone,Y., Kira,A., and Hayashizaki,Y.	
TGTTGAAG 2317 GGTTTCTG 2681	TITLE JOURNAL MEDLINE PURMED	RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913	
SCCTGTAC 2141 SAGCCGGA 2437 SGCCGGA 2801 SGCCCGA 2801 ATGCCCTCA 2497 SCCTCAGTC 2861	AUTHORS	Kawai,J., Shinagawa,A., Shibata,X., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Kombo,H., Adachi,J., Fukuda,S., Atzakawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,J., Satico,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Satico,R., Adatsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,M., Gasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pasole,G., Gudechenban,J., Schrinh,L.M., Stabuli,F., Suzuki,R., Tomita,M., Mashio,T., Sakubi,K., Okido,T., Furuno,M., Anno,H.,	
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I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The dT-tailed vector was circularized with E. coli DNA ligase after digestion of EcoRT which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof* by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."	Ouery Match 15.8%; Score 456.4; DB 12; Length 625; Best Local Similarity 99.8%; Pred. No. 2.7e-116; Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 1210 TGAPTTARTGACAGAMAGATTGAGACAGCATCTTAGATTGACTGACTTGA	1290 TATATGTTCCTCGAAAGATGGGACCCTGTGACCCCCCCCC	1410 CATTGCCCATGACTCGAACAATTTGGCATGATGAAGATTAGAGATTAGGACTGGCCTTCAC 1410 CATTGCCCATGACTCTGGAACATTTGGCATGATTGAAGAAAGA	03 0350 03	RESULT 5 BM845044 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS RM845044.1 GI:1920143 KINWORDS RST RST RGT RGT RGT RGT RGT RGT RGT RGT RGT RG	REFERENCE 1 (Dases 1 to 623) AUTHORS KM,N.S., Hahn,Y.', Oh,J.H.', Lee,J.Y.', Ahn,H.Y.', Chu,M.Y.', Xim,M.R.', Oh,J.H.', Lee,J.Y.', Ahn,H.Y.', Chu,M.Y.', Cheong,J.E.', Sohn,H.Y.', Kim,J.M.', Park,H.S.', Kim,S. and Kim,Y.S.' Cheong,J.E.', Sohn,H.Y.', Kim,J.M.', Park,H.S.', Kim,S. and TITLE 21C Frontier Korean EST Project 2001 JOURNAL Unpublished Contect: Kim YS Contact: Kim YS Genome Research Center Korea Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
	Db 1889 GACCACGTTTGAATACCGTTCCTTTAACGGCCTCTAACGACGCTATGCACCAGAC 1948 Oy 2618 CAACCAACGACACTACTGGAGCGTGTTTTCAGGAAGGAACGACGGGTGTTGCC 2677 Ob 1949 CCACGAATGAGACGTGTTTGAGAATTCTGAGAAAACGGGGGATCGCGGTTT 2008	Oy 2679 GGGAATACTCCATGCCTCGCTTGGGGACGGAGAAGCAGCCCCTGCCCAGCCCAGCT 2734 Db 2009 GHAHT CACTTCCCAAGGTCATAATAATAACTCAAGCCACCACCAAGAATAACCAC 2068 Qy 2735 ACACTTGGGCCATCGAGTCTGAGTCCTGCGGAGGGGGGT 2784 Db 2069 ACACTTGGGCATCTGACTGAGTCTCAGTCATCCTGCGGAGGGGGT 2784 Db 2069 ACACTTGGCGCACATGATCTGACTGATCACCTGCGGTGGAGGT 2118	RESULT 4 HMS50160 BMS50160 BMS50160 BMS50160 BMS50160 BFINITION RY-ESCIOL30714 S128NU216 Homo sapiens CDNA clone S128NU216-81-C06 5', mRNA sequence. BMS501601 GI:19206559 KEYWORDS EST. SWMSTON HOME Sapiens (human) ORGANISM HOME Sapiens (human)	Bukaryota, Metazoa, Chordata, Craniata, Mammalia, Eutheria, Primates; Catarrhini (Gases 1 to 625) Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ah (Dh, K.J., Cheong, J.E., Sohn, H.Y., Kim, Y.S., Cheong, J.E., Sohn, H.Y., Kim, J.M. (Contact: Kim YS Genome Research Center	Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Vuscong-gu, Daejeon 305-33, South Korea Fai: 48-42-860-4409 Fax: +82-42-860-4409 Email: yongsungsmail.kribb.re.kr Place: 81 row: C column: 06 High quality sequence stop: 62. High quality sequence stop: 62. Coranism."Homo sapiens." // organism."Homo sapiens." // dolum: 1.479e="MRNA" // dolum: 1.479e="MRNA" // dolum: 1.479e="MRNA" // dolum: 1.479e="MRNA" // dolum: 1.479e="MRNA" // dolum: 1.479e="MRNA" // dolum: 1.479e="MRNA" // single - MRNA" /	/tissue_type="Lymph node" /cell_type="Epithalial" /cell_type="Epithalial" /lab_Rost="Toplor1" /lab_Rost="Toplor1" /loore="Oxgan: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: Not!; The Poly (A)+ RNA was dephosiphorylated with bacferial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (BAP). The decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Invitrogen
TobNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Libri at:
Futp://maga-lihi.gov
Plate: LiAM1287 row: n column: 11
High quality sequence stop: 728.
Lication/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="S12SNU216-97-E10"
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Fax: +82-42-860-4409
Fax: 97 row: E column: 10
High quality sequence stop: 633.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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                                                        1782 TATGCCAGCAGCAGAAGGCACAATTTGTGGGGATGACATGTGGTGCCGGGGAGGACAGTG 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2082 GCACAACAGCAGACGATTCAGAGGCGGCACTACAAGTGGAAGCCTTACACTCAAGTAGA 2141
                                                                                                                                                                                                                                                                    1902 TTGGTCCCCATGCTCCAGGACCTGCGGAGGGGAGTATCTCATAGGAGTCGCCTCTGCAC 1961
                                                                                                                                                                                                                                                                                                                                                                       1962 CAACCCCAAGCCATCGCATGGAGGGAAGTTCTGTGAGGGCTCCACTCGCACTCTGAAGCT 2021
                                                                                         311 TATGCCGCAGCAGAAGGGACCGTTTGTGGCTTGAGTATGTGGTCTCGGCAAGGCCAGGTG 370
                                                                                                                                                          1842 TGTGAAATATGGTGATGAAGGCCCCAAGCCCACCCATGGCCACTGGTCGGACTGGTCTTC 1901
                                                                                                                                                                                        551 GYĞCAATATTAACCCTTĞCAATGAAATAĞCTTĞĞATTTTCĞĞĞĞCTCAAÇAĞTĞTĞĞAĞA 610
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251 GAAGGATATTTGCAAATCACTTTGGTGCCACCGAGTGGGCCACAGGTGTGAGACCAAGTT 310
                                                                                                                                                                                                                                                                                                                  491 TAACCCCAARCCTCAGTATGGTGGCATATTCTGTCCAGGTTCTAGCCGTATTTATCAGCT
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Fax: +82-42-860-4409
Email: yougsungemail.kribb.re.kr
Email: yougsungemail.kribb.re.kr
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/clone_lacknra"/clone sphens Placknra"
/clone="vector: powsesory 6, 1st strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-trand cDNA was digested with Not I and cloned
double-trand cDNA was digested with Not I and cloned into
library was not normalized. Ill others
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Genoscope - Centre National de Sequencage
BP 191 91006 ENRY Cedex - France
BP 191 91006 ENRY Cedex - France
Email: SequeGegenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8035.r For
more information about this cluster, see
http://www.genoscope.cns.fr, cluster, see
About Cluster.cgl?seq=CSONEONIGIQPI&cluster=8035.r. Contact;
Ferg Librar Email: Eliangalifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Ayanue, Genoscope, sequence ID : CSONEONIDGILQPI.
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                                                                                  319 GAAGGAACCCGGGIGITGCCTGGGAATACTCCATGCCTCGCTTGGGACCGAGAAGCAGC 378
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                             Contract: Robert Strausberg, Ph.D.

Email: Gapba-romail nih.gov.

Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares. University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MC clone distribution information can be
found through Lib I.M.A.G.E. Consortium/LUNL at:

http://image.llnl.gov.
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                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Musinae, Mus. (bases 1 to 698) NM-MG, Mgc. ncl.nih.gov/. NM-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was contributed by the Brain Molecular Anatomy Project
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5709081"
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Location/Qualifiers
Mus musculus (house mouse)
Mus musculus
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UT-M-EXC-bxj-1-10-0-UI.xI NUH-BHAP_EXO Mus musculus CDNA clone
IMAGE:5709081 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 CTGGTCACCCCGCAGCCGCCAGTATCTACAAATTTCTAAGCACCGCTCAAGCTATCTG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 CATTGCCCATGAGTCTGGACACATTTGGCAFGATTCATGAGAAGGGAACATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 TATATGTTCCTGGAAGAATGAGCCCTGTGACACTTTGGGATTTGCACCCATAAGTGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; Score 368.4; DB 12; Length 537; 99.7%; Pred. No. 1.2e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S12SNU216-99-B04"
                                                                                                                                                                                                                                            /tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SNU-216"
/lab_host="Top10F"
/clone_lib="S12SNU216"
                                                                                           organism="Homo sapiens"
   High quality sequence stop: 537.
                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ444190
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Homo sapiens
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa, Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 323)
Bulas Neto, B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva, W. Ur., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de doliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF933693 332 bp mRNA linear EST 22-JAN-2001 IJ5-NT0228-211200-358-e08 NT0228 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         965 GTATAGATGGGATATGTGAGCTCAGTGTGGTGTCCACATCTG-CGCACATGCCCCAGCCT 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1084 TCTCTTCTGAGGTCCCATAGAATGAAGAACTGAACGTGGAGACCTTGGTGGTGGTGGTCGAC 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1144 AAAAAGATGATGCAAAA-CCATGGCCATGAAATATCA-CCACCTACGTGCTCACGATAC 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          667 CGATCACACAGAAACTCGCCATCGCATGGAGGGAAGTTCTGTGAGGGCTCCACTCGCACT 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ČGAŤCAČAČAČAĀAČTČCTČA--------GTGGČČCTŤTCAĀČC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727 CTGAAGCTCTGCAACAGTCAGAAATGTCCCCGGGACAGTGTTGACTTCCGTGCTGCTCCTCAG 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 TGCCAAGGCTTGTCAGGCATGATAGGAACAGAAGAGGCAGATTACTTCCTAAGGCCACTT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                787 TGTGCCGAGCAÇAACAGCAGACGATTCAGAGGGCGGÇACTAÇAAGTGG--AAGCCTTACA 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 creracaadaarccacadagccccargcrccrosgcccagrcagccrosgccrccrosgccrc- 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905 TITCTITGICAAATAAAGTCAAAGAFGGGACTCCATGCTCGGAGGATAGCCGTAATGTTT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 ------AAGGACATGGGAGTTGGCATCAACCCCTGCACAGCAGCACCTTCGC 504
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488 CCGAGGTTGAGTCTCTTCACCTTGAAAGGCCCCCAGGCACGACTTCCACATGGATC
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                                                                                                                                                                                      61 CCGAGGTTGAGTCTCTTCACCTTCGGCTGAAAGCTCCAGGCACCACGACTTCCACGTGGATC
                                                                                                                                                                                                                                                                                 548 TGAGGACTTCCAGCAGCCTAGTGGCTCCTGGCTTTATTGTGCAGACGTTG-GGAAAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1122 bp mRNA linear EST 12-MAR-2002
SV, mRNA sequence.
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        1538 CCTGCAGCCGCCAGTATCTACACAAATTTCTAAGCACGCTCAAGCTATCTGCCTTGCTG 1597
                                                                                                                                           1598 ATCAGCCAAAGCCTGTGAAGGAATACAAGTATCCTGAGAAATTGCCAGGAGAATTATATG 1657
                                                                                                                                                                                                                                                                                 1658 ATGCAAACACACAGTGCAAGTGGCAGTTCGGAGAGAAAGGCAAAAGTCTGCATGCTGGACT 1717
                                                                                                                                                                                                                                                                                                                                                                                                                            1718 TTABABAGGACHTCTGTABAGCCCTGTGGTGCCATCGTATTGGAAGGAAATGTGAGACTA 1777
                                                                                                                                                                                                            467 ATGAGCCCAAGCAAACGCGACAGTATAAATATCCGGACAACTCCCGGGACAGATTTATG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 TTATGAAGGACATTTGCAAGTCACTCTGGTGCCACGCGTGGGCCACAGATGTGAAACCA 646
                                                                         527 ATGCCGACATGCAATGTAAGTGGCAATTTGGAGCCAAAGCCAAGCTGTGCAGCCTTGGGG 586
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1122)
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National Institutes of Health, Mammalian Gene Collection (WGC)
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|Mol_type="mRNA"|
| Ab xref="taxon:9606"
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| Ab host="taxon:9606"
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Contact Labradoury for Computational Genomics
Considiated Labradoury for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
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                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,W.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/mol_type="mRNA"
/strain="Sprague-Dawley"
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/clone="U1-R-FU0-cpx-h-14-0-UI"
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Rattus norvegicus
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This is appeared by the FAPESP/LICR Human Cancer Genome Project. This equence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-NT0228-211200-358-e08&t5=2000-12-21&t4=1)
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Labozatory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp.
                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Pred. No. 8,6e-81;
                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                 Simpson, A.J.
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bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (IAP) and then decapped
intact mRNA was ligated with DNA-NNA linker including EcoR
I site by treatment of T RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
primming with dT-tailed vector. The CDNA vector was
adjusted to have about 60nt. The CDNA vector was
adjusted to have about 60nt. The CDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
competent cells E. coli ToplOF' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched CDNA library."
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1 (bases 1 to 657)
Sarou, Y., Shini, T., Kohara, Y. and Sarou, N.
Expressed genes in Ciona intestinalis (2002c)
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Location/Qualifiers
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Contact: Nori Satoh
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Fax: 81-75-705-1113
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                              1650 ATTATATGATGCAAACACACAGTGCAAGTGGCAGTTCGGAGAAAGCCAAGCTCTGCAT 1709
                                                                                                                                                                               1770 TGAGACTAAATTTATGCCAGCAGCAGCAGGCACAATTTGTGGGCATGACATGTGGTGCCG 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1830 GGGAGGACAGTGTGTGAAATATGGTGATGAAGGCCCCAAGGCCACCCATGGCCACTGGTC 1889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 GCAAGGCCAATGTGTAAAGGCTTGGAGATCTCGGGCCCCGGCCCATCCACGCCCAGGGTGGTC 490
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordates, Catarrhini, Hominidae, Homo.

In (bases 1 to 410)

Kim.N.S., Hahn,Y., Oh.J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.

Kim.N.S., Hahn,Y., Oh.J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.
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Korea Research Institute of Bioscience & Biotechnology
Sorena-dong Vuseong-gu, Daejeon 305-333, South Korea
Tel: +682-42-860-4470
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/clone="S12SNU216-91-A08"
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/cell_type="Epithelial"
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Email: yongsungsmail.kribb.re.kr
Plate: 91 row: A column: 08
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Location/Qualifiers
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                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                         1244 AAGATGGGACTCGTCATGACCACGCCATCTTACTGACTGGTCTGGATATATGTTCCTGGA 1303
                                                                                                                                                                                                                                                                                                                                                                 1304 AGAATGAGCCCTGTGACACTTTGGGATTTGCACCCATAAGTGGAATGTGTAGTAATATATC 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1364 GCAGCTGCACGATTAATGAAGATACAGGTCTTGGACTGGCCTTCACCATTGCCCATGAGT 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .424 CTGGACACAACTTTGGCATGATTCATGATGGAGAAGGGAACATGTGTAAAAAGTCCGAGG 1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1724 AGGA-----CATCTGTAAAGCCCTGTGGTGCCATCGTATTG---GAAGGAAATGTG 1771
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 greacataardicacedaecergaarddaectaarddrefrariteaegregieneraerigra 311
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                                                                                                                                                                                                                                                                                                                                                                                                         72 AGAATAAACCATGTGAAACATTAGGGTTGGCGCAAATAGGAGGAATGTGCAGTGAACGCA 131
                                                                                                                                                                                                                                                                                                                   12 AATTCGGCACGAGGCCCGATCACTCAATTCTGTTAACTGGTATCGATATGCGTGGATA 71
                                                                 /tissue type="gomad"
/cione lib-Nori Sorio unpublished cDNA library, gonad"
155 c 178 g 161 t others
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                              12;
                                                                                                                                                                             8.2%; Score 237; DB 13; Length 657; 62.9%; Pred. No. 9.4e-55;
                                                                                                                                                                                                                              0; Mismatches 226; Indels
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/mol_type="mRNA"
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Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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Nature 409 (6821), 685-690 (2001)
High-efficiency full-length cDNA cloning
                                                          Meth. Enzymol. 303, 19-44 (1999)
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AFGODLHIEURSSA1LSSFIPRVQLGNGSASTREPSTPQCLYGGTRUDSSSSVNVS
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GGGTGRPRRSAGKSQNGLNVFTLVVADAROVJEKHGKDDVTTY1LTVVNMVSSLFKDGTI
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/procein_id="8Ac29190.1"
/db_xref="61:26330920"
/rranslation="MECALLCLCALRAAGPGPPWGPAGLGRLAKALQLCCFCCASVAV
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DICSWINDEDDILEPRIPIGGOKSKYRSCTINBDTGLGLAFTIAHESGHNFGWVHDGBG
NPCRRADGNINGPTJGSNIGPSWSSCSRQYLKRTRTPROLAFIJG**
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                                                                                            cDNN library was prepared and sequenced in Mouse Genome EDN Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Wilhittp://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-63-503-9216)
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                                                                                                                                                                                                                     prepare mouse tisques
Please visit our web site for further details.
Please visit our web site for further details.
URL: http://fantom.ggc.riken.go.jp/.
URL: http://fantom.ggc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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Search completed: October 28, 2003, 23:23:11

Job time : 5382 secs

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                                                            October 28, 2003, 18:26:52; Search time 194 Seconds
                                                                                                                                                                                                                                                                                        1: /cgm2_6/pcodata/2/ina/5A_covB.seq:*
2: /cgm2_6/pcodata/2/ina/5B_covB.seq:*
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4: /cgm2_6/pcodata/2/ina/6B_covB.seq:*
5: /cgm2_6/pcodata/2/ina/PcrUS_covB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 3, Application US/09930872
| Patent No. 644838
| Patent No. 644838
| GBNERAL INFORMATION:
| APPLICANT: Friddle, Carl Johan
| APPLICANT: Hilbun, Erin
| TITLE OF INVENTION: No. 6483886el Human Proteases and Polynucleotides Encoding the FILE REPERROR: LET APPLICANTON NUMBER: US/09/930,872
| CURRENT APPLICATION NUMBER: US/09/930,872
| CURRENT APPLICATION NUMBER: US 60/225,852
| PRIOR PILING DATE: 2000-08-16
| NUMBER OF SEQ ID NOS: 5
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                                                   Sequence
US-09-122-1268-1
US-09-634-286A-1
US-09-62-451-346
US-09-62-451-346
US-09-598-326-346
US-09-128-158-16
US-09-39-333-20
US-09-39-333-20
US-08-39-333-12
US-08-39-333-12
US-08-39-333-12
US-09-539-333-12
US-09-539-333-12
US-09-130-491-7
US-09-130-491-7
US-09-671-317-485
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US-09-128-158-158-158-178-185
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2.5 3001
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2.4 4 2014
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ORGANISM: homo sapiens
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Db S67 TCCTCAGTGGCCCTTTCAACCTGCCAAGGCTTGTAACCTGCCAAGGCTTGTAACAACAACAACAACAACAACAACAACAACAACAACAAC	920 980 831 1039 951 1159 9611	6, Db 1071 TTATTCAAAGA CAATAGGAGGAAACATCAACATTGTAGGTCTGATTCTT CT 261	273 DD 441 DD 326 QY 501 DD 386 QY 137 446 QY 621 DD 506 QY 681 DD 566 QY 681 DD 566 QY 741 DD 742 DD 681 DD 1551 741
2653 CAGGGAAGGAACCGGGTGTTGCTGGGAATACTCCATGCCTGGCTTGGGGACCGAAAG 2553 CAGGGAAGGACCGGTGTTTGCTGGGAATACTCCATGCCTGGCTTGGGGACCGAAAG 2553 CAGGGAAGAACCGGGTGTTGCCTGGGAAAACTCCATGCCTTGGGAACGAAGAAG 2773 CAGCCCTGCCTAGCCTAGCTACACTTGGGCATCGTGCCTTGAGACCTGTGTGCCTTGAGACCGTGTCC 2553 TGCGGAGGGGG 2783 2553 TGCGGAGGGGG 2783	NESULT 2 US-09-910-872-5 US-09-910-872-5 Sequence 5, Application US/09930872 Sequence 6, Application US/09930872 Sequence 6, Application US/09930872 GENERAL INFORMATION: APPLICANT: Fridale, Carl Johan APPLICANT: Fridale, Carl Johan APPLICANT: Fridale, Carl Johan APPLICANT: Hilbun, Erin TTLE OF INVENTION: NO. 644838881 Human Proteases and Polynucleotides Enc TILE OF INVENTION: NUMBER: USA CURRENT FILING DATE: 2001-08-14 PRIOR PELING DATE: US 60/225,852 PRIOR PLING DATE: US 60/225,852 PRIOR FILING DATE: US 60/225,852 PRIOR FILING DATE: US 60/225,852 PRIOR FILING DATE: Windows Version 4.0 SEQ ID NOS: 5 SEQ ID NOS:	Query Match 64.8%; Score 1874.6; DB 4; Length 4042; Bast Local Similarity 94.4%; Pred. No. 0; 1 1 1 1 245; Gaps 245; Gaps 245; Gaps 245; Gaps 245; Gaps 1	

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802 AGCAGACGATTCAGAGGGGGGCACTACAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG 859
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ORGANISM: homo sapiens
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                                                                                                                                           CATCACATGTGGTGCCGGGGGGGCAGTGTGTATTGGTGATGAGGCCCCAAGCCC 1850
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1693 AAAGCCAAGCTCTGCATGCTGGACTTTAAAAAGGACATCTGTAAAGCCCTGTGGTGCCAT 1752
                                                               CGTATTGGAAGGAATGTGAGACTAAATTTATGCCAGCAGAAGAGAAGCAAATTTGTGGG 1812
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Sequence 1 Application US/09930872
Parcer No. 644838
Parcer No. 644838
Parcer No. 644838
APPLICANT: Priddle, Carl Johan
APPLICANT: Hilbur, Erin
TITLE OF INVENTION: No. 64488881 Human Proteases and Polynucleotides Encoding the PIE REPERBRUE. LEX-0219-USA
CURRENT FILING DATE: 0001-08-14
CURRENT FILING DATE: 2001-08-14
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NOS: 5
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22.0%; Score 663; DB 4; Length 1476;
Best Local Similarity 71.5%; Pretc. No. 1.46-180;
Marches 1079; Conservative 0; Mismarches 185; Indels 245; Gaps
2773 TGCGGAGGGG 2783
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Patent No. 639589
GENERAL NO. 639589
APPLICANT Robison, Keith E.
TITLE OF INVENTION: NOTIFIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEASE HOMOLOGS
FILE REFERENCE: 5800-55
CURRENT APPLICATION NUMBER: US/09/192,184
CURRENT FILING DATE: 1999-09-09
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50.9%; Pred. No. 2.4e-48;
ive 0; Mismatches 714; Indels 44; Gaps
                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(5357)
OTHER INFORMATION: reprolysin (ADAM family of metalloprotease)
NAME/KEX: misc_feature
LOCATION: (1)...(5357)
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-392-184-5
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Matches 787; Conservative
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ORGANISM: Homo sapiens
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3199 GCCGAGGGCCTGGGGTATGTGGATGTGGGGGTGATCCCAGCCGGCGCACGCGAGATCCGC 3140
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350 CAGGCCTGCCCTGCTGGCCGCCCCTCCTTCCGCCACGTCCAGTGCAGCCACTTTGACGCT 3491
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Sequence 6, Application US/09369364A
Batent No. 6391610
GENERATION
APPLICANT: Apte, Suneel
APPLICANT: HURSAINEN, Tina L.
APPLICANT: HURSAINEN, Tina L.
APPLICANT: HIRORAE, Satoshi
TITLE OF INURNICAN: NUCLEIC Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/40017/10-30-00
CURRENT APPLICATION NUMBER: US/09/569,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOSTWARE: PREMETIN Ver. 2.1
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US-09-364A-6
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TYPE: DNA ORGANISM: Homo sapiens ADAMTS-7
                                                                      ; NAME/KEY: CDS
; LOCATION: (13)..(3003)
US-09-369-364A-6
LENGTH: 3218
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1486 réccacacacrerderécrete---resonacereterentenancements 1542 1258 CATGACCACGCCATCTTACTGACTGGTCTGGATATATGTTCCTGGAAGAATGAGCCCTGT 1317 1372 AAGGACATTATCGÁCTTCCCCTCGGTGCCACCTGGCGTCCTATGATGTAAGCCACCAG 1431 1432 idececenceagiacosoceraeneneereneesiidasgassacanssanansie 1485 1732 TGTAAAGCCCTGTGGTGCCATCGTATTGGAAGGAAATGTGAGACTAAATTTATGCCAGCA 1791 1792 GCAGAAGGCACAATTTGTGGGCATGACATGTGGTGCCGGGGACGACAGTGTGTGAAATAT 1851 1543 GTGGACGGCACCCGGTGTGGGGAGAATAAGTGGTGTCTCAGTGGGGAGTGCGT---ACCC 1599 1852 GGTGATGAAGGCCCCAAGCCCACCCATGGCCACTGGTCGGACTGGTCTTCTTGGTCCCCA 1911 1600 Gradacriccedecededeceracardaracricardacradacacacardarecara 1659 1912 TGCTCCAGGACCTGCGGAGGAGGAGTATCTCATAGGAGTCGCCTCTGCACCAACCCCAAG 1971 1660 TGCTCACGGAGCTGTGGCATGGGCGTACAGAGCGCGAGCGGCAGTGCACGCAGCCTACG 1719 1780 chásocrásocrastrásocs contecrio carcarcar con contra de contra con 1839 2212 GTCAAAGATGGGACTCCATGCTCGGAG-----GATAGCCGTAATGTTTGTATAGATGGG 2265 1954 TGTGTGGATGGCACCCCTGCTACCAGGTCCGAGCCAGCCGGGACCTCTGCATCAACGGC 2013 1318 GACACTTIGGGATTTGCACCCATAAGTGGAATGTGTAATAATATCGCAGCTGCACGATT 1377 1075 gagaccerdogacitoreceargingecodocardifeceagecococococococococococo 1134 1438 GGCATGATTCATGGAGAAGGGAACATGTGTAAAAAGTCCGAG-----GGCAACATC 1491 1195 GGCATTCAGCATGACGGAAGCGGCAATGACTGTGAGCCCGTTGGGAAACGACCTTTCATC 1254 1492 ATGTCCCCTACATTGGCAGGACGCAATGGAGTCTTCTCCTGGTCACCCTGCAGCCGCCAG 1551 1255 Archereckanacrentarasakanasakantakanakarakarakandakan 1314 TATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCCTTGCTGATCAGCCAAAGCCT 1611 1315 TATATCACCAGGTTCCTTGACCGTGGGGCCTGTGCCTGGACGACGCTCT---GCC 1371 TGCAAGTGGCAGTTCGGAGAGAAAGCCAAGCTCTGCATGCTGGACTTTAAAAAGGACATÇ 1731 1972 CCATCGCATGGAGGGAAGTTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGT 2031 1720 CCCAAAIACAAAGGCAGAIACTGTGTGGGTGAGCGCAAGCGCTTCCGCCTCTGCAACCTG 1779 2032 CAGAAATGTCCCCGGGACAGTGTTGACTTCCGTGCTGCTCAGTGTGCCGAGCACAACAGC 2091 2092 AGACGATTCAGAGGGCGGCACTACAAGTGGAAGCCTTACACTCAAGTAGAAGATCAGGAC 2151 1840 ATGCTCTACAAGGGCCAGCTGCACACATGGGTGC-----CCGTGGTCAATGACGTGAAC 1893 1894 CCCTGCGAGCTGCCGCCCGCCCGGGAATGAGTACTTTGCCAAGAAGCTGCGGGACGCC 1953 1015 carcacraccarcerecreaceasascacererecearcascearcasces 1378 AATGAAGATACAGGTCTTGGACTGGCCTTCACCATTGCCCATGAGTCTGGACACTTT 1612 GTGAAGGAATACAAGTATCCTGAGAAATTGCCAGGAGAATTATATGATGCAAACACACAG Gaps Query Match
6.3%; Score 182.6; DB 4; Length 3218;
Best Local Similarity 50.6%; Pred. No. 3:8e-42;
Matches 714; Conservative 6; Mismatches 699; Indels 42; 1552

1420 GAGTCTGGACCACATTGGCATGATTCATGATGGAGAAGGGAACATGTGT 1470 1108 GAGATCGGGCACACATTGGCATGATCATGATGGAGAACATGTGT 1470 1108 GAGATCGGGCACACATTGGCATGACGGCGTGGGAACATGTGT 1167 1471 AAAAGTCGGGCACACATCATGCCTACATTGGCAGGAACCAGTGTGGGGCCGT 1167 1108 GGTCAGGACCCAGCACATCATGACTGCCACATTACCATGAAGACCAACCCATTGCC 1530 1128 TGGTCACCCTGCAAGCTCATGACACATTTCTAAGACCCGACCCATTGC 1580 1228 TGGTCACCCTGCAACCTGTACACACATTTCTAAGACCGGCCCAAGCTTTGC 1580 1280 CTTGCTGCAACCGTGAACACATACACATTTCTAAGACTGGGAAATTCCCAGGAAATTCCAGGAAATTCCAGGAAATTCCAGGAAATTCGAGAAATTCGAGAAATTCGAGAAATTCGAGAAATTTCAAGAAACAACAAGCAATCGCATGGAAAAAAAGAACAACAAACA	1456 ATCACCAACACCCCGGCGCGGAGGGCCCCCCAACGCCCCCCC
8 6 8 6 8 6 8 6 8 6 8 6	8
Qy 2266 ATMTGTGAGAGAGTTGGATGCATGGATCTGATGCTGTTGAAGAGGTCTGT 2326 Db 2014 ATCTGTAAGAGACTTGAGGTTGACGATTGACGAGTGTATGAGGAGGACCGTGT 2038 Qy 2326 GGGGTGTAAGGGGTTGACGATTCACGAGGACTATCACGAGGACCTAAGGAGCCGTGT 2386 Db 2074 GGGGTGTAAGGGAATAACTCAGCCGACCACCGTGAGGAGCCCGAGGACCCAGGAGG 2130 Qy 2386 CACCACACCACCAACGACACGCTCACTCCACCTCCACCTCCACGGAGGCCGAGATCCCC 2445	RESULT 6 US-09-364-16 US-09-364-16 Sequence 16, Application US/09369364A Sequence 16, Application US/09369364A Sequence 16, Application US/09369364A Setent No. 6391610 GENERAL INFORMATION: MARCHART APPLICATION NUMBER: US/09/369, 364A TITLE OF INVENTION: UNALES OF 1399-08-06 CURRENT APPLICATION NUMBER: US/09/369, 364A NUMBER OF SEQ ID NOS: 31 SEQ ID NO 18 SEQ ID NOS: 31 SEQ ID NO

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2137 GTAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAGAAGGATTTGATTTCTTCTTT 2196
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
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; Patent No. 6428998
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REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 938
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STREET: 11
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                                      2542 CGGTACAARITITCGGGCACTACTITCGACTACAGACGGTCCTATAATGAGCCCGGAGAAC 2601
                                                                                                                  2233 cercreccerciaecredeaccácerircáacreceácaegescagaccaégrecadas 2292
2482 GTGCGCAATGCCCTCAGAAGGTACTACCTGAATGGGCACTGGACCGTGGACTGGACTGGCCCGGC 2541
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APFLICANT: Morelann, Tina L.
APPLICANT: Hurskainen, Tina L.
APPLICANT: Hichata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REPERENCE: 2673/4007/10.30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
OGREDIANT PRIMICATION NUMBER: 1999-08-06
SEQ ID NOS: 31
SOFTWARE: PARENT UNC. 2.1
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                                                                                                                                                              2602 TIAATCGCTACTGGACCAACCAACGAGACACTGATTGTGGGAGCTGCTG 2649
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48.5%; Pred. No. 4.5e-31;
tive 0; Mismatches 481; Indels 11
                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09369364A Patent No. 6391610
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ORGANISM: Homo sapiens ADAMTS-6
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LOCATION: (1169)
CTHER INFORMATION: n = C
NAME/KEY: misc feature
LOCATION: (1620)
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US-09-369-364A-4
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LOCATION: (22)..(2601)
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     US-09-369-364A-4
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2317 GACGTCTGTGGGGGTGTGTAACGGGAATAACTCAGCCTGCACGATTCACAGGGGTCTCTAC 2376
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                                                                                                                                                                    1867 gaacgrgcrccrgccgcrgarcgargggacccagrgcaargcggarrcacrgcgararcrdc 1926
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1807 ggágsrggggtaaaaccrrgrgcarraaacrgcrrgggrgaaggraaagriaraarricracacr 1866
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                                                                                       2197 ICTITGICAAATAAAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGT
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APPLICANT: Laptere, Charles M.
APPLICANT: Laptere, Charles M.
APPLICANT: Prockep, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF ENGUREES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows
SOFWHARE: FastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
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2022 GCACCGGGATGCCAAGGAGAGATGCCACCTGTACTGCGAGTCCAGGGAGACCGGGGAGGT 2081
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650-493-5556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                     4,1%; Score 118.4; DB 4; Length 2450;
48.0%; Pred. No. 9,6e-24;
tive 0; Mismatches 591; Indels 30;
LEBEAX: 660-493-4935
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LEBGTH: 2450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOCY: linear
                                                                                                                                                                                                                                                                                 Best Local Similario,
Matches 573; Conservative
                                                                                                                                                                                                                                                                              Local Similarity
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2193 CTTTTCTTTGTCAAATAAAGTCAAAGATGGGACTCCATGCTC---GGAGGATAGCCGTAA 2249
                                                                         2082 GGTGTCCATGAAGCGCATGGTGCATGATGGGACGCGCTGCTCCTACAAGGACGCCTTCAG 2141
                                                                                                                                                   2250 TGTTTGTATAGATGGGATATGTGAGAGGTGGGATGTGACAATGTCCTTGGATCTGATGC 2309
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APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockep, Darwin J.
TITLE OF INVENTION: RECOMBINANT N. PROYEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 17
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OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FastEBC for Windows Version 2.0b
CURRENY APPLICATION BATA: US/09/491,522
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    Pønnie & Edmonds, LLP
1155 Avenue of the Americas

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APPLICATION NUMBER: 08/886,333
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Patent No. 6428998
GENERAL INFORMATION:
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REGISTATION NUMBER: 30,605
REPERENCE/DOCKET NUMBER: 838
TELECOMMUNICATION INFORMATION:
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2262 CACGITCACACGGTCACCCAAGAAGCATGCTTACATCAAGATGTTTGAGATCCCTGCAGG 2321
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: 1155 Avenue of the Americas
New York
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APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                        Sequence 9, Application US/09491522; Patent No. 6428998; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 2450 base pairs
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Matches 570; Conservative
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ADDRESSEE: Pennie & 1
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                                                                                                                                                                                                     US-09-491-522-9
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2430 AGCCCGGAGTATCCGCATCTATGAAATGAACGTCTCTACCTCCTACATTTCTGT 2483
                                                                                  2322 AGCCAGACACCTGCTCATTCAGGAGGTAGACGCCACCACCACCATCTGGCCGT 2375
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APPLICANT: Lopker, Charles M.
APPLICANT: Lopker, Charles M.
APPLICANT: Recombination N.
TITLE OF INVENTION: RECOMBINAT M-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
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17.8%; Pred. No. 1.5e-22;
Ive 0; Mismatches 593; Indels 30;
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OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
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Darwin J.
RECOMBINANT N-PROTEINASE,
AND THE PRODUCTION, METHODS AND USES THEREOF
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SOFWHARE: FASSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
FILING DATE:
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1155 Avenue of the Americas
New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
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REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
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INPORVATION POR SEO ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 4580 base paire
TYPE: mucleic acid
STRANDENESS: single
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Matches 570; Conservative
APPLICANT: Frockop, Dara
TITLE OF INVENTION: RECC
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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                                              1543 AGCCGCCAGTATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCCTTGCTGATCAG 1602
                                                                                                               1473 Adccagcadascridasccecriaccriccrarca-----cridcriccescardac 1526
                                                                                                                                                                                                   1603 CCAAAGCCTGTGAAGGAATACAAGTATCCTGAGAAATTGCCAGGAGAATTATATATGATGCA 1662
                                                                                                                                                                                                                                                                     1527 cccrrcac---ccaccaccaccacccacccagerccccagerocccagerocccageraccare 1583
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3.9%; Score 114.2; DB 4; Length 4580;
47.8%; Pred. No. 2.2e-22;
tive 0; Mismatches 593; Indels 30;
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Sequence 8, Application US/09491522 Patent No. 6428998 GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.

US-09-491-522-8

Gaps 33;

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1271 AAAGTGTAGTCGAAAATATATCACTGAGTTTTTAGACACTGGTTATGGCGAGTGTTTGCT 1330
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                                                                                                                                                                                                                                                                                           974 AGGIGGAAICCAICAICAIGAIACIGIICICIIIAACAAGACAGGAIAICIG---CAGAGC 1030
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                                                                                                                                                       Length 5804;
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                                                                                                                                                          Query March 3.9%; Score 113.6; DB 4; Best Local Similarity 47.7%; Pred. No. 3.8e-22; Marches 542; Conservative 0; Mismatches 561;
                   CTHER INFORMATION: n=T
NAME/KEY: misc feature
LOCATION: (1563)
CTHER INFORMATION: n=T
US-09-369-364A-12
  COCATION: (1406)
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                                                                                     AAGAAGGGGCCACCCTGGATGGGACCATGTGTGCGCTGGCAAGCACTGCTTTAAAGGA 1763
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.644 TTCGACCCGTGCAAACAGCTGTGGTGCAGCCACCCTGACAACCCCTACTTTGCAAGACA 1703
                                                                                                                                                                                                                                                        AGTCCCTTCGGCTCCTGCTGCTGCGGCACAGGTGTGAAGTTCAGGACCCGTCAG
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                                              AAATTTATGCCAGCAGCAGAAGGCACACTTTGTGGGCATGACATGTGGTGCCGGGGAGGA
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| Patent No. 6391610
| GRNERAL INFORMATION:
| GRNERAL INFORMATION:
| APPLICANT: Apre. Sunce1
| APPLICANT: Hircheat, Sactoshi
| TITLE OF INFORMATION: NUCLEIC AcidE Encoding Zinc Metalloproceases;
| TITLE PREPARED: 199-08-06
| CURRENT FALICATION NUMBER: US/09/169,364A
| CURRENT FALICATION NUMBER: US/09/369,364A
| SOFTHARE: Patentin Ver. 2.1
| SEQ ID NO. 12
| LENGTH: 5804
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ORGANISM: Homo sapiens ADAMTS-9
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SOFTWARE: PatentIn version 3.0
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1865 CCCTAAATACAGTGGAATTCTGATGAAGGACCGGTGCAAGTTGTTCTGCAGAGTGGCAGG 1924
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APPLICANT: Agte, Suncel
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hirobata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloprotesses
FILE REPERBNCS: 26473/4007/10.300-00
CURRENT APPLICATION NUMBER: US/08/369,364A
CURRENT FILING DATE: 1999-08-06
SOFTWARE: Patentin Ver: 2.1
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; Sequence 1, Application US/09369364A
; Patent No. 6391610
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; LOCATION: (18)..(2810)
US-09-369-364A-1
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LENGTH: 3002
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1763 GGAAATGTGAGACTAAATTTATGCCAGCAGAAGGCACAATTTGTGGGGCATGACATGT 1822
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RESULT 14

RESULT 14

Sequence 13, Application US/09445023A

Sequence 13, Application US/09445023A

Sequence 13, Application US/09445023A

Sequence 13, Application US/09445023A

SEPLICANT HAROZAKION:

APPLICANT: Inhoka, Keiko

APPLICANT: Ishioka, Keiko

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANTON: Human ADANTS-1 protein, gene encoding the same, pharmaceutical

TITLE OF INVENTION: composition and method of immunologically analyzing human ADANT:

CURRENT FILING DATE: 1999-12-03

FRIOR APPLICATION NUMBER: US/09/445,023A

CURRENT FILING DATE: 1999-12-03

FRIOR APPLICATION NUMBER: US/09/445,023A

WUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91) CATGGGGACCGTGGGGAGACTGCTCAAGAACCTGTGGTGGTGGAGTTCAATACACAATGA 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1031 GAGAATGTGACAACCCAGTCCCAAAGAACGGAGGGAAGTACTGTGAAAGGAACGAGGTCC 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1151 AGCAGTGCGAGGCGCACAATGAGTTTTCCAAAGCTTTCGGAATGAGCCCACTGTAG 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1211 AGTGGACACCCAAGTACGCCGGCGTCTCGCCAAAGGACAGGTGCAAGCTCCACCTGTGAAG 1270
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                                                                                                                                                                                                                                                                                                              1433 ACTTTGGCATGATTCATGATGGAGGAAGGGAAC------ATGTGTAAAAAGTCCG 1480
                                                                                                                                                                                                                                                                                                                                                                                                1481 AGGGGAACATCATGTCCCCTACATTGGCAGGACGCAATGGAGTCTTCTCCTGGTCACCCT 1540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1661 CAAAÇACACAÇAGTGCAAGTTÇGGAĞAGAAAGÇÇAAGÇTÇTGCATGCTGG--AÇTT 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1719 TAAAAAGGACATCTGTAAAGCCCTGTGGTGCCATC-GTATTGGAAGGAAATGTGAGACTA 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1778 AATTTATGCCAGCAGCAGAAGGCACAATTTGTGGGCATGACATGTGGGTGCCGGGGAGGAC 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1892 ACTGGTCTTCTTGGTCCCCATGCTCCAGGACCTGCGGAGGGGGGAGTATCTCATAGGAGTC 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1952 GCCTCTGCACCAACCCCAAGCCATGGAGGGAAGTTCTGTGAGGGCTCCACTCGCA 2011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2064 TGCTGCTCAGTGTGCCGAGCACAACAGCAGATTCAGAGGCGGCACTACAAGTGGAA 2123
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                                                                                                                                              1313 CCTGTGACACTTTGGGATTTGCACCCATAAGTGGAATGTGTAGTAAATATCGCAGCTGCA 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1838 AGTGTGTGAA----ATATGGTGATGAAGGCCCCAAGCCCACCCATGGCCACTGGTCGG 1891
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                                                                                                                                                                                     377 CGTGTGACACTCTCGGAATGGCAGATGTTGGAACCGTATGTGACCCCAGCAGCAGCTGCT 436
                                                                                                                                                                                                                                                                       437 CAGTCATAGAAGATGATGGTTTGCAAGCTGCCTTCACCACAGCCCATGAATTGGGCCATG 496
                                                                                                                                                                                                                                                                                                                                                   497 TGTTTAACATGCCGCACGATGATGCTAAGCACTGTGCCAGCTTGAATGGTGTGGGG 556
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                                                       Match 3.5%; Score 101.2; DB 4; Length 2184; Local Similarity 48.3%; Pred. No. 8e-19; Local Similarity 48.3%; Pred. No. 9e-19; Alsmatches 53; Indels 51;
j LOCATION: (1)..(2184)
US-09-445-023A-13
                                                                                 Best Local Simmatches 564;
                                                               Query Match
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NAME/KEY: unsure

LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681

COTHER INFORMATION: a, t, c, g, or other

US-09-484-9708-58
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2294 TCCTTGGATCTGATGCTGTTGAAGACGTCTGTGGGGTGTGAACGGGAATAACTCAGCCT 2353
                                                                                                                         1391 TCATAGACTCCAAAAAGAAGTTTGATAAGTGTGGCGTTTGTGGAGGAACGGTTCCACAT 1450
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                                                                                                                                                                                        1451 ĠĊAAĠAAGATGTCAĠĠAATAGTĊĀĊTĀ-----GTACAĀGACCTGGĠTĀTCĀTGĀĊĀTTĞ 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1430 ACAACTTTGGCATGATTCATGGAGAAGGGAAC------ATGTGTAAAAAGT 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER_INFORMATION: Incyte ID No. 6426186 007074.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Oones, Karen A. APPLICANT: Volkmuth, Wahlen B. APPLICANT: Volkmuth, Wahlen B. APPLICANT: Walker, Michael G. TITLE OF INVENTION: BONE REMODELING GENES FILE REFRENCE: PE-0014 US CURRENT FAILNO DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                        2414 TCACCATTCCTTCTGGAGCCCGGAGTAT 2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 58, Application US/09484970B
; Patent No. 6426186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE; DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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QY 1715 DD 940 QY 1775 DD 1000 QY 1889 DD 1120 QY 1949 DD 1240 QY 2066 DD 1360 QY 2118 DD 1420 QY 2171 DD 1420 QY 2231 QY 2351 DD 1540 QY 2351 DD 1600	S ACTITAAAAAGSACATCTGTAAAGCCCTGTGGTGCCATCGTATTGGAAGGAA	S CTAAATTTATGCCAGCAGAGAAGGCACAATTTGTGGGGATGACATGTGGTGCGGGGAG 1834 	GACAGTGTGTGAAATATGGTGATGATGACCCCAAGCCCACCCATGGCACTGGT 1888 	OCGACTIGETETTETTGGCCCCATGCTCCAGGACCTGCGAGGGGGGTATCTCATAGGA 1948 GAATGTGGGGGGCTTTGGGGAGACTGTTCGAGAACGTGCGGTGGGGGGGG	OGTOGCCTCTGCACCCAAACCATGCATGGAGGGAAGTTCTGTGAGGGCTCCACTC 2008	2009 GCACTCTGAAGCTCTGCAACAGTCAGAAATGTCCCCGGGACAGTGTTGACTTCCGTG 2065 1240 TGCGCTACAGATCTGTAACCTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAG 1299	CIGCTCAGTGTGCCGAGCACAACAGCAGAGGAGAGGGGGGCACTACAA 2117 AGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGGCTGGGG 1359	GIGGAAGCCTTACACTCAAGTAGAAGATCAAGACTTATGCAAACTCTACTGTA 2170 	TOGGAGAATTIGATTICTICTITICTITIGICAAAAAGICAAGATGGGACTCCAT 2230 	GCTCGGAGGATAGCCGTAATGTTTGTATAGATGGGATATGTGAGAGTTGGATGGTGACA 2290	2291 ATGTCCTTGGATCTGATGCTGTTGAAGACGTCTGTGGGGTGTAACGGGAATAACTCAG 2350 	CCTGCA 2356 CTTGTA 1605

Search completed: October 28, 2003, 23:26:41 Job time : 208 secs

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(without alignments)
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17: /cgn2_G/pcdata/2/ubbna/USG_PUB_COMB_seq:*
                                                                                                                                                                                                  October 28, 2003, 18:50:06 ; Search time 751 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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2895
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 3, Appli	Sequence 1, Appli	2,	7	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 8689, Ap	Sequence 22417, A	Sequence 1437, Ap		Sequence 1, Appli	ý	Sequence 23, Appl	Sequence 1, Appli	Sequence 2, Appli
SUMMARIES			ID	US-10-217-774-3	US-10-296-616-1	US-10-217-774-5	US-10-240-545A-1	US-10-226-560-1	US-10-226-560-3	US-10-217-774-1	US-10-029-386-8689	US-10-029-386-22417	US-09-833-381-1437	US-10-103-377C-3	US-10-103-377C-1	US-10-226-560-6	US-09-963-791-23	US-09-963-791-1	US-09-788-043C-2
			80	13	15	13	12	14	14	13	12	12	10	14	74	14	10	10	70
			Match Length DB	3675	3675	4042	3666	2589	3013	1476	525	348	339	2052	2377	2217	2274	2727	2879
	de	Query	Match	64.8	64.8	64.8	24.5	23.3	23.3	22.9	10.1	10.1	9.2	9.2	9.5	8.3	7.8	7.8	7.8
			Score	1874.6	1874.6	1874.6	708	673.4	673.4	663	292.8	292.6	267.4	265.8	265.8	241.2	227	227	227
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Sequence 4, Appli Sequence 10, Appli Sequence 10, Appl Sequence 8, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	1,4,0,4,1		Sequence 1056, Ap Sequence 3, Appli Sequence 21, Appl Sequence 11, Appl
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ALIGNMENTS

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Sequence 3, Application US/1021774
PRULACATION NO. US2000193593A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
FILE REPERENCE: LEX-0210-USA
CURRENT FILING DATE: 2002-08-12
PRIOR FILING DATE: 2002-08-12
PRIOR FILING DATE: 2002-08-12
PRIOR FILING DATE: 2002-08-12
PRIOR FILING DATE: 2000-08-16
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1491 CGCAATGGAGTCTTCTCCTGGTCACCCTGCAGCCGCCGGTTTCTAAGC 1550 1573 ACGCTCAAGCTATCTGCCTTGCTGATCAGCCAAGCCTGTGAAGGAATACCAAGTATCT 1612 1561 ACGCTCAAGCTATCTGCCTTGATCAAGCCTGTGAAGGAATACCAGTATCCT 1610 1633 GAGAATTGCCAGAGAATTATTGATCCAAACCCAGTGCAGGATACCAGTTCCGAGGA 1692 1611 1 1 1 1 1 1 1 1	1791 CATCARCHIGHCGACGACAGAACAGTCTGAAATATGGTGATGAAGGCCCCAAGCCC 1850 1873 ACCCATGGCCACTGGTCGACTGTCTTGGTCCATGCTCAGACCCCCAAGCCC 1850 1873 ACCCATGGCCACTGGTCGACTGGTCTTCTTGGTCCCCATGCTCCAGGACCTGCGGAGGG 1932 1851 ACCCATGGCCACTGGACGTCGTCTTCTTGGTCCCCATGCTCCAGGACCTGCGGAGGG 1910 1893 GGAGTATCTCATAGGAGTCGCCTTGCACCACCCCAAGCCATGGAGGGAAGTTC 1970 1993 TGTGAGGGCTCCACTGGACTCTGCACCAACAGTCAAAATGTCCCGGGAAGTTC 1970 1993 TGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAAAATGTCCCGGGAAGTTC 1970 1974 GTTGAACATCCCTGACTCTGAAGCTCTGCAACAGTCAAAATGTCCCCGGGACAGT 2030 2043 GTTGAACTTCCCTCACTCTCTAAATGTCCCCAACAGTCAAAAATGTCCCCGGGACAGT 2030	2031 GTTGACTTCCGTCCTCTCATGTCCCGAGCACACGCGATTCAGGGGCCGCCC 2090 2113 TACAAGTGGAACCTTACACTCAAGTAGAAGATCAGGACTATCAGGGGCCGCCC 2090 2103 TACAAGTGGAAGCCTTACACTCAAGTAGAAGATCAGACTTATGCAAACTCTACTGTATC 2175 2091 TACAAGTGGAAGCCTTACACTCAGTAGAAGATCAGACTTATGCAAACTCTACTGTATC 2125 213 GCAGAAGGATTTCATTCTTTTCTTTGTCAAATAAAGATCAAAGATGGGACTCCATGC 2212 2151 GCAGAGATTTCATTTCTTTTTTTTTTTTTTTAAAAGATCAAAATGAGACTCCATGC 2210 2233 TCGCAGGATTTCATTTTTTTTTTTTTTTTTTTAAAGATCAAAATGAGAACTCCATGC 2210 2233 TCGCAGGATTACCTTTTTTTTTTTTTTTTTTTTTTTTAAAGATCAAATGATCAATTAAAACTCCATGC 2210 2233 TCGCAGGATTACCTTTTTTTTTTTTTTTTTTTTTTTTTT	2211 drictricharicrichichach Grictrichgederichtakoeselarhacheket
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CCAGGAGCAGGACAGTTCGGAGAGAACCCAGGACAGATTTATGGGAGCAGAGTTTATAAAAAAACCCAAGAGTTTATAAAAAACCCAAGAGTTTATAAAAAACCCAAGAGTTTATAAAAAAAA	2393 ATTACCTCAACGGGGCTGAACCTGACTGGGCGGGGGGAAAATTTCGGGGACTA 2553 21933 ATTACCTCACGGGGCTGGAGCATGACTGGCCTGGGGAGAATTTTCGGCTGGGACTA 2553 2564 CTTTCGACTACAGGGGCTGGAGCATGGCCTGGCGGGAACTTACCCTTCGCTGGCAACCA 2553 2564 CTTTCGACTACAGGGCTCTTTCAACGCCCCGGAACGTTGCTACTGGCCCAGGGCCCACAA 2512 2453 CTTTGATACCACGCTTTTCAACGCCCCGGAACGTCGTACGGCCCAGGGCCCACAA 2512 2513 ATGAGACGTGGTTTTGA 2531 2513 ATGAGAGGTGGTTTTGA 2531
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2594 ACCCAGCACCCCCCAGAACCCAGAACCCCCCCCCCAAAACCACC	Qy 1424 CTGGACACAACTTGGCATGATTCATGATGACAAGGAACAGGAACAGGAACAGGTGTAAAAAGTCCGAGAAGGTGAAGGATGAGTGTGTAAAAGGTGATGATGATG

US-10-226-560-3 Sequence 3, Application US/10226560 Publication No. US200300504641 GENERAL INCORMATION: GENERAL INCORMATION: APPLICANT Hu, Yi APPLICANT Hu, Yi APPLICANT Hu, Yi APPLICANT Friddle, Carl Johan TITLE DE INVENTION: No. US20030050464Nel Human Proceases and Polymucleotides Encodir TIEE REPRENCE: LEx-0372-USA CURRENT APPLICATION NUMBER: US/10/226,560 CURRENT FILING DATE: 2002-08-22 PRIOR PILING DATE: 2001-08-22 PRIOR PILING DATE: 2001-08-22 PRIOR PILING DATE: 2000-07-28 NUMBER OF SEQ ID NOS: 6 SOFTWARE: RealESQ for Mindows Version 4.0 SEQ ID NO 3 ITVEE DATE: 2010 TYPEE DATE TITLE DATE: 2010-07-28 NUMBER OF SEQ ID NOS: 6 SOFTWARE: RealESQ for Mindows Version 4.0	1784 2056 1844 2116 1904 2176 2236 2024 2024
; ONOMINIO SAPLEIIS US-10-226-560-3	2356
Query Match 23.3%; Score 673.4; DB 14; Length 3013; Best Local Similarity 65.6%; Pred. No. 2.16-202; Matches 997; Conservative 0; Mismatches 521; Indels 1; Gaps 1124 AGACCTIGGRGGTGGTCGAAAAAAGATGGAAAACCATGGAAAATATCACA 11397 AAACGGGTTGTGGTGGTGAATATCTGTGGAAAACGAGAACTGGAGGATTATTGATAAAATGGGGA 1184 CCTAGCTGGTCAAGATGCTCAAATGCTGCTTTATTCAAAATGGGGGA	Qy 2144 ATCAGGACTTATGCAAACTCTACTGTATGCAGAAGGATTTGATTTCTTTTCTTTGT 2203 Db 2416 AGGAAGATGAAGTGTACTGCAAGGCGGAAGAATTTTTTTT
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Oy 1604 CARAGCCTGTGAAGGATACCTGAGAATTGCCAGGAGATTTATGATGCA 1663 Db 1876 CCAAGCAGGACAGTATAAATTCCGGACAAACTACCAGGACTTATAGATGCTG 1935 Oy 164 ACACACAGTGCAAGTGCCAGGACAGAAACTGCAGAGCATTATAGAGCTTTAAA 1723 Db 1936 ACACACAGTGTAAATGGAAAACCCAAAAGCCAAGATTTGGAAGACTTATGCAGCCTTGGTTTTGTGA 1995 Oy 1724 AGGACATCTGTAAAGCCCTGTGCTGCATAGGAAAATTGGAAGACAAATTATGAAGAAATTATGAAGAAATTGAAAGAAA	RESULT 7 US-10-217-774-1 Sequence 1, Application US/10217774 Publication No. US20020193583A1 GENERAL INFORMATION: APPLICANT: Fiddle, Carl Johan APPLICANT: Hilbur, Erin TITLE OF INVENTION: Same TITLE OF INVENTION: Same FILE REPERBUCE: LEX-0219-USA CURRENT APPLICATION NUMBER: US/10/217,774

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OTHER INFORMATION: MAP TO AC022424.3

CHER INFORMATION: EXPERSESED IN BONE MARROW, SIGNAL = 0.81

OTHER INFORMATION: EXPERSESED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
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22.9%; Score 663; DB 13; Length 1476;
Best Local Similarity 71:5%; Pred. No. 2.7e-199;
Matches 1079; Conservative 0; Mismatches 185; Indels 245;
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CURRENT FILING DATE: 2002-08-12
PRICE APPLICATION UNNBER: US/09/930,872
PRICE FILING DATE: 2001-08-14
PRICE APPLICATION UNBER: US 60/225,852
PRICE FILING DATE: 2000-08-16
NUMBER OF SEC ID NOS: 5
SSOFIUMARE: RESISEQ for Windows Version 4.0
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ORGANISM: homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Pank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hansel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILLE OF PROPLICATION UNDERS. 195/10/029,386
CURRENT APPLICATION NUMBER: 195/10/029,386
CURRENT PELING DATE: 2001-12-20
SOTTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ. ID NOS: 34288
SOTTWARE: Annomax Sequence Listing Engine vers. 1.1 US-10-029-386-8689/c ; Sequence 8689, Application US/10029386 ; Publication No. US20030194704A1 ; GENERAL INFORMATION:

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1579 CAAGCIAICTGCCTTGCTGATCAGCCAAAGCCTGTGAAGGAATACAAGTATCCTGAGAAA 1638
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Patent No. US20020132090A1
CENERAL INFORMATION:
APPLICANT EODISON, Keith B.
TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT PATION: NO. US20020132090A1e1 Nucleic Acid and Protein Homologs
CURRENT PATION: NO. US20020132090A1e1 Nucleic Acid and Protein Homologs
CURRENT FILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1437
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                                                                    TTCGGCTGAAAGGCCCCCAGGCACGACTTCCACATGGATCTGAGGACTTCCAGCAGCCTAG 568
                                                                                                      Tresecrehadecrecadecacoactrecacardearcreadeactrecadeacerae 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1875 CCATGGCCAC-TGGTCGGACTGGTCTTCTTGGTCCCC 1910
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US-09-833-381-1437
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LOCATION: (1)...(339)
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US-09-833-381-1437
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US-10-103-377C-3
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                                                                                                                                  10.1%; Score 292.8; DB 12; Length 525; 96.2%; Pred. No. 6.2e-82; ive 0; Mismatches 12; Indels 0;
       OTHER INFORMATION: EXPERSED IN FETAL LIVER, SIGNAL = 2.7
OTHER INFORMATION: SWISSPROT HIR: 015072, EVALUE 2.00e-08
OTHER INFORMATION: NT HIT: A2296304.1, EVALUE 5.00e-08
US-10-029-386-88689
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OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FIFAL LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN FIFAL LIVER, SIGNAL = 2.7
OTHER INFORMATION: MISSPROT HIT: P97857, EVALUE 3.00e-07
OTHER INFORMATION: WILSPROT HIT: AU296304.1, EVALUE 3.20e-01
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FEATURE:
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Matches 420; Conservative
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; LOCATION: (323)...(2374)
US-10-103-377C-1
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                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 2377
RESULT 12
US-10-103-377C-1
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                APPLICANT BANGATY, Rejasekhar
TITLE OF INVENTION: 65577 A Human Marrix
TITLE OF INVENTION: Metalloproteinase and Uses Therefor
                                                                   FILE REPRENCE: MPIOL-049PIRM
CURRENT APPLICATION NUMBER: US/10/103,377C
CURRENT FILINO DATE: 2002-08-26
PRIOR APPLICATION WUMBER: 60/278,347
PRIOR FILING DATE: 2001-03-23
                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: CDS
LOCATION: (1) ... (2055)
US-10-103-377C-3
    GENERAL INFORMATION:
                                                                                                                                                                                                                              2052
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                                                                             ; Sequence 1, Application US/10103377C; Publication No. US20030073098A1; GENERAL INFORMATION:
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APFLICANT: Turner, C. 34 Cander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Scoville, John
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T. 02002120113Alel Human Proteases and Polynucleotides Encod
FILE REPRENUE: LEX.0105-105A
                   1935 ACAGTATAATATCCGGACAAACTACCAGGACAGATTTATGATGCTGACACACAGTGTAA 1994
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PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FRALEEQ FOr Windows Version 4.0
SEQ ID NO 23
LENGHH: 274
TYPE: n. 274
                                                                                                                                                                                                                                                                                                          , Sequence 23, Application US/09963791
; Patent No. US20020120113A1
; GENERAL INFORMATION:
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Sequence 6, Application US/10226560

Sequence 6, Application US/10226560

Sequence 7. US2030050464A1

GENERAL INFORMATION:

APPLICANT: Walker 10.

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APPLICANTON: NO. US20030050464A1e1 Human Proteases and Polynucleotides Encodir:

CURRENT FPLING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: US 60/314,049

PRIOR APPLICATION NUMBER: US 60/314,049

PRIOR APPLICATION NUMBER: US 60/21,644

PRIOR APPLICATION NUMBER: US 60/21,644

NUMBER OF SEQ ID NOS: 6

SOCTUMER: PASEESQ for Windows Version 4.0

LENGTH: 2217
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64.5%; Pred. No. 3.8e-65;
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2303 GAGACGCTGGTCTTTGA 2319
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Best Local Similarity 64.5
Matches 419; Conservative
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CORGANISM: homo sapiens
US-10-226-560-6
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                                                                                                                                    NUMBER OF SEQ 1D NOS: 25
SOFTWARE: FARCSEQ for Windows Version 4.0
SEQ 1D NO 1
LENGTH: 2727
CURRENT APPLICATION NUMBER: US/09/963,791
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,769
PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-791-1
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Patent No. US2002012011331
GENERAL INFORMATION:
APPLICANT Donoho, Gregory
APPLICANT Turner, C. Alexander Jr.
APPLICANT Turner, C. Alexander Jr.
APPLICANT Seconifie, John
APPLICANT Seconifie, John
APPLICANT Seconifie, Datan
APPLICANT Sendes, Arthur T.
TITLE OF INVENTION: No. US2020120113Alel Human Proteases and Polynucleotides Encodir
FILE REPERENCE: LEX-0105-USA
        1178 AGGGAGATGIGITCCTITTGGCACTIGGCCCCAGAGCATAGATGGGGCTGGGGTCCCT 1237
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1871 GIGCAGACTITGACAATAIGCCTITCGAGGAAAGIATTATAACTGGAAACCGAATACT-	AAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATGGCAGAAGGATTTGATTTCTTCT	gsaggragaggggggggggggggggggggggggggggg	TITCITIGICAAATAAAGICAAAGATGGGACTCCAIGCICGGAGGATAGCCGTAAIGITT	cronacorocreciosociantes de contraciones de con	GTATAGATGGGATATGTGAGAGAGTTGGATGTGGAAGGAAGTGGGTGGT	Argerage	AAGACGTCTGTGGGGTGTGTAACGGGAATAACTCAGCCTGCACGATTCACAGGGGTCTCT		ACACCAAGCACCACCACCAACCAGTATTATCACATGGTCACCATTCCTTCTGGAGCCC	Teatgattcactgcccagggaggctacatggaggtggggagatacagaggctctg 2227	GGAGTATCCGCATCTATGAAATGAACGTCTCTACCTACATTTCTGTGCGCAATGCCC	TTCACATTGAAGTTAGAGAAGTTGCCATGTCAAAGAACTATATTGCTTTAAAATCTGAAG	TCAGAAGGTACTACCTGAATGGGCACTGGACCGTGGACTGGCCGGCC	2288 GAGATGATTACTATATTAATGGTGCCTGGACTATTGACTGGCCTAGGAAATTTGATGTTG	CGGGCACTACTTTCGACTACAGACGGTCCTATAATGAGCCCGAGAAACTTAATCGCTACTG 2614	2348 crosoacacritircariacaasaccaacroatdaaccakarcciiosaascrcias	2615 GACCAACCAACGAGACACTGATTGTGGAGCTGCTGTTTCAGGGAAGGAA	2408 GTCCTACCTCAGAAAATCTCATCGTCATGGTTCTGCTTCAGAACAGAATTTGGGAATT	
TGGAAAC	GGATTTG	GGTTATA	GATAGCO	SATTCAC	GGATCTG	scarcre	SATTCACA	rgccattg	SATICCIT	SATACCAA	rrcrgrgc	rgctttaa	GGCCGGT	raggaaat	SAACTTAA	arcchige	AAGGAACC	ACAGAATT	
 ATTATAAC	TCGCAGA	recercan	SCTCGGAC	SCAATGC	ATGICCII	ATATTT	CCTGCACC	cargread	TGGTCAC	TGGTGCAC	CCTACAT	ACTATAT	ACTGGCC	ACTGGCC	AGCCCGAC	AACCAGA	TTCAGGG/	TTCAAGA	
 GGAAAGT.	TACTGTA	AACTGCT	SACTCCAT	sacceagn	ATGTGACA	rergara	PACTCAG	GGAAGCA	rtatcaca	CATGGAAG	CTCTACCT	JI GTCAAAGA	SACCGTGG	SACTATTG	CTATAATG	aactgatd	screener	GGTTCTGC	
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 AATATGC	GACTTAT	AAACCTT	AAAGTCA	geedrek	TGTGAGA	TGCAAGC	GTGTGTA	sercrere	CACACCA	SCCCAGGG	TATGAAA	FAGAGAAG	CTGAATG	rattaatg	GACTACA	rcartaca	SACACTGA	AAATCTCA	
 CTTTGAC	AGATCAG	srdgggra	GTCAAAT	srecreci	ATGGGATA	TGGAGA	rcreres	SATGTCGA	AGCACCAC	ATTCACTO	rcccar	TTGAAGT1	GGTACTA	ATTACTA	CTACTIT	CAGCTTT	CCAACGA	CCTCAGA	
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GenCore version 5.1.6
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Human ADAM-TS 7-li	protease		Human ADAM-TS-like	Human aggrecanase	NOVX related prote	Human protease (NH	metallo	Novel human protea	metallo	ın protea	encoding	related	related	related	related	related	Human protease-rel	metallo	27875	Human ADAM type me	27875		metal	Human aggrecanase	DNA encoding prote	Muman metalloprote	ADAM	Homo s		Human metalloprote	polyp	aci	met		Human protein modi	
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23	23	23	23	23	24	24	23	24	22	22	23	24	24	24	24	24	22	22	22	22	22	23	23	23	23	23	22	53	23	23	23	53	53	21	24	
856	1236	1021	556	1221	1162	862	934	491	959	908	1120	353	353	353	349	353	757	1690	1686	1686	1686	1044	1044	1104	1103	1103	1103	1104	1133	1132	1103	1068	1068	1784	852	
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ALIGNMENTS

376	AC ABG76897;	05-NOV-2002		·		KW neurodegeneration; Parkinson's disease; pain; stroke; endometriosis;	•									KW ileal sodium/bile acid cotransporter; prohibitin; MT; CIP4; spinesin;	
							 			 		 					KW gap junction beta-5 protein; hepsin/plasma transmembrane serine protease. XX
							-	-	-	 	-	 -	 -	 _	_	_	

MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS

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Best Local Similarity 100.
Matches 952; Conservative
                                                               Query Match
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The present invention relates to new NOVX (NOV1-10) polypeptides. The molecules of the invention are useful for treating or preventing a NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, or a disorder related to cell signal processing and metabolic pathway modulation in humans. NOVX polypeptides, nucleid acids and antibodies are useful for treating or preventing disorders or syndromes including breast cancer, Alzheimer's disease, epilepsy, Huntingron's disease, anxiety, behavioural disorders, multiple sclerosis myasthenia gravis, neurodegeneration, Parkinson's disease, pain, stroke, autoimmune disease, allergises, addiction's asthma, endometriosis, graft versus host disease, systemic lupus erythematosus, scleroderma, transplantation, psortasis, Cronn's disease, HUN (buman immunodeliciancy virus) infection, psortasis, cronn's disease, theumatodia strhitis, diabetes, thromborytopenia, bleeding disorders, metabolic disorders, obesity, glucose transport defect, glometrioned arthitis, dispetes, bestitus, schorestinal disorders, and disorders, had disorders, had disorders, had disorders, had disorders, had disorders, intextinal disorders, congenital diarrhoea, respiratory disease, pastro-intestinal disorders, urinary system disorders, respiratory disease, pastro-intestinal disorders, urinary system disorders, viral, beamatopoietic disorders, urinary system disorders, viral, bacterial, or parasitic infections.

The present amino acid sequence represents a NOVX protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheimer's disease, cardiomyopathy, metabolic disease and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edinger S, Gerlach V, MacDougall JR, Malyankar UM, Smithson G;
Miller I, Peyman JA, Stone DJ, Gunther E, Ellearman K, Shimkets RA,
Padigaru M, Guo X, Patturajan M, Taupier RJ, Burgess CE;
Pertusen BD, Kekuda R, Spytek KA, Gangolli EA, Fernandes ER;
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100.0%; Pred. No. 0;
ive 0; Mismarches
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                                                                                                                                                                                                                                     2000US-241058P
2000US-241063P
2000US-242152P
2000US-242482P
2000US-242481P
2000US-242611P
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20010S-26913P.
20010S-286324P.
2001US-294108P.
2001US-303698P.
2001US-0981151.
                                                                                                                                        17-OCT-2001; 2001WO-US32496
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17-0CT-2000; 2
20-0CT-2000; 2
23-0CT-2000; 2
23-0CT-2000; 2
24-0CT-2000; 2
24-0CT-2000; 2
24-0CT-2000; 2
28-DEC-2000; 2
28-DEC-2000; 2
28-DEC-2000; 2
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16-OCT-2001;
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Gaps ő

Indels

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240 300 360 420 361 LRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNWVSALFKDGLMGKDGTRHDHA 420 480 540 540 900 999 099 FCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYC 720 720 780 780 840 900 120 180 300 360 PLFSAGTCVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ 120 9 PEKLPGELYDANTQCKWQFGBKAKLCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTIC GHDMWCRGGQCVKYGDEGPRPTHGHWSDWSSNSPCSRTCGGGVSHRSRLCTNPKPSHGGK IABGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNS ACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTV 1AEGFDFFFSLSNKVKDGTPCSEDSRNVC1DG1CERVGCDNVLGSDAVEDVCGVCNGNNS 781 ACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTV PLESAGICVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENO ILLIGLDICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIH GHDMMCRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGK MKPRARGWRGLAALHMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS TLHVLTQYDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL RTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL RISSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFS 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFFS LSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSL LRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDGLMGKDGTRHDHA DGEGNMCKKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAGAICLADQPKPVKEYKY DWPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAWEYSMPRLGTE 952 KOPPAQPSYTWAIVRSECSVSCGGRCLPVLLLEAACQPSATAYIALAFLES ABG76894 standard; Protein; 986 (first entry) 05-NOV-2002 661 661 721 721 841 301 541 601 781 ABG76894; 63 61 121 181 181 241 301 361 421 481 481 601 903 901 RESULT 2
ABG76894
ID ABG70
XX
AC ABG70
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XX 셤 g ò g 셤 ઢ g ð S S 셤 à 쉱 원 à g 셤 Š 셤 à g ò 셤 ò ò ò à à à g a ò

Human zinc matalloprotease-like protein #1.

KW mast cardiomyopathy; atherosclerosis; cell signal processing; breast cancer, Alzabamer's disease; pellepsy; Hunington's disease; pellepsy; Hunington's disease; pellepsy; Hunington's disease; pellepsy; Hunington's disease; pellepsy; Hunington's disease; pellepsy; Hunington's disease; Mw anxiety, behavioural disease; allergy addiction; asthms; transplantation; graft versus host disease; Hill frection; human imminodeficiency virus; we profit size to confine disease; Heumatoid arthritis; diabetes; panceatitis; thrombocytopenia, bleeding disorder; metabolic disorder; poseity; thrombocytopenia, bleeding disorder; metabolic disorder; poseity; who proyestic kindry disease; remail tubular acidosis; skin disorder; metabolic disorder; poseity; who manatopoistic disorder; point disorder; poseity; who mental disease; dental infection; growth disorder; reproductive disorder; metalloptocases, dental infection; growth disorder; reproductive disorder; when metalloptocases, phWm-TS 7; alpha-Camcroglobilin precursor; metalloptocases, phWm-TS 7; alpha-Camcroglobilin precursor; metalloptocases, phWm-TS 7; alpha-Camcroglobilin precursor; metalloptocases, phWm-TS 7; alpha-Camcroglobilin precursor; metallopticase, phWm-TS 7; alpha-Camcroglobilin precursor; metallopticase, phWm-TS 7; alpha-Camcroglobilin precursor; metallopticase, phWm-TS 7; alpha-Camcroglobilin precursor; metallopticase, phWm-TS 7; alpha-Camcroglobilin precursor; metallopticase protein; hepsin/plasma transmembrane serine protease; metallopticases protein; hepsin/plasma transmembrane serine protease; metallopticases, dentallopticases, dentall

Homo sapiens

Location/Qualifiers Misc-difference

/note= "Arg substituted by Gly as a result of a single nucleotide polymorphism (SNP)" /note= "Ala substituted by Pro as a result of a single Misc-difference 158

Misc-difference 373
/note= "Val substituted by Ala as a result of a single nucleotide polymorphism (SNP)" nucleotide polymorphism (SNP)"

Misc-difference 553 /note= "Cys substituted by Arg as a result of a single nucleotide polymorphism (SNP)"

WO200233087-A2.

25-APR-2002.

17-OCT-2001; 2001WO-US32496

23-OCT-2000; 2000US-242612P. 24-OCT-2000; 2000US-242880P. 24-OCT-2000; 2000US-242881P. 2000US-241063P. 2000US-242152P. 2000US-242482P. 2000US-242611P. 2000US-241058P 23-OCT-2000; 23-OCT-2000; 17-CCT-2000; 17-OCT-2000;

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(CURA-) CURAGEN CORP.

2001US-303698P. 2001US-0981151

09-JUL-2001;

16-OCT-2001;

29-DEC-2000; 2000US-259028P. 25-APR-2001; 2001US-286324P. 29-MAY-2001; 2001US-294108P. Gerlach V, MacDougall JR, Malyankar UM, Smithson G; Peyman JA, Stone DJ, Gunther E, Ellerman K, Shiakets RA; Guo X, Patturajan M, Taupier RJ, Burgess CB; D, Kekuda R, Spyrek KA, Gangolli EA, Pernandes ER; Millet I, Pey Padigaru M, G Zerhusen BD, Edinger S, Gorman L;

439 LGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPT 498

-----GLMGKDGTRHDHAILLTGLDICSWKNEPCDT 438

408 -----

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The present invention relates to new now (NOVE NOVE) pupped lass. The molecules of the invention are useful for treating or preventing a molecules of the invention are useful for treating or preventing a disorder related to cell signal processing and metabolic pathway a disorder related to cell signal processing and metabolic pathway a disorder related to cell signal processing and metabolic pathway cer useful for treating or preventing disorders and antibodies are useful for treating or preventing disorders including breast cancer, Albahaman disorders, multiple sclerosis, mystehenia gravis, neurodegeneration, Parkisnon's disease, pain, stroke, autoimmune armiery, behavioural disorders, multiple sclerosis, graft versus host disease, altergies, addiction, asthma, endomerriosis graft versus host disease, systemic lupus erythematous scleroderma, transplantation, psoriasis, Crohn's disease, HV (human immunodeficiency virus) infection, psoriasis, Crohn's disease, HV (human immunodeficiency virus) infection, compenital distriboea, respiratory disease, gastro-intestinal diseases, musele, home, joint and skeltezt disorders, proceders, pancrearitis, renal tubular acidosis, skin disorders, congenital distribus, proceders, hamentoders, musele, home, joint and skeltezt disorders, manalomer, disease and infection, curinary bystem disorders, osteoporosis, dental disease and infections. The present amino acid sequence represents a NOVK protein of the 61 PLFSAGTCVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ 120 61 PLFSAGTCVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ 120 181 RTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL 240 181 RISSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL 240 KLCNSQKCPRDSVDFRAAQCAEHNSRRPRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFS 300 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEXDLCKLYCIAEGFDFFFF 300 301 LSNKVKDGTPCSEDSRNVC1DGICELSVVSTSAHMPQPPKEDLFILPDEXKSCLRHKRSL 360 301 LSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSL 360 361 LRSHRNEELNVETIVVVDXXXMAQNHGHENITIYVLTILMMVSALFXD----- 407 Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleix acids encoding the polypeptides for diagnosing and treating nucleix acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alkheimer's disease, cardiomyopathy, metabolic disease and e.g. cancer. 121 TLHVLTQYDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL 121 TLHVLTQYDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL 1 MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS 1 MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS The present invention relates to new NOVX (NOV1-10) polypeptides. The 50; 97.6%; Score 5110; DB 23; Length 986; 94.6%; Pred. No. 0; iive 1; Mismatches 3; Indels 50; Claim 1; Page 14; 305pp; English. Local Similarity 94.6 nes 940; Conservative WPI; 2002-590434/63. 986 AA; N-PSDB; ABS59323 invention. Sequence Query Match 241 diabetes Matches ద ò 윱 යි g ದ್ದ à 유 ð à à ò

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541 LAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKWQ 600
                                                                                                                                                                                                                                                               679 RDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDG 738
                                                                                                                                                                                                                                                                                                                                                      721 RDSVDFRAAQCAEHNSRRFRGRHYKWKP-----QDLCKLYCIAEGFDFFFSLSNKVKDG 774
                                                                                                                                                                                                                                                                                                                                                                                                              739 TPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQY 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                    775 TPCSEDSRNVCIDGICE-XGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-H 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        859 YNEPENLIATGPTNETLIVELLFQGRNPGVAWEYSMPRLGTEKQPPAQPSYTWAIVRSEC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKWQ 558
                                                                                                                                                      FGEKAKLCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTICGHDMWCRGGQCVKYGDEG 618
                                                                                                                                                                                               601 FGEKAKLCMLDFKKDICKALWCHRIGRKCETKFWPAAEGTICGHDMWCRGGQCVKYGDEG 660
                                                                                                                                                                                                                                          619 PKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGSTRTLKLCNSQKCP 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             833 YHMVIIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRRS
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ABG76895 standard; Protein; 791 AA. RESULT 3 ABG76895

ABG76895;

05-NOV-2002 (first entry)

Human zinc matalloprotease-like protein #2.

Human, NOVX; cardiomyopathy, atherosclerosis; cell signal processing;
Whereast cancer, Albrahmer's disease; pall-paps, Huntington's disease;
anxiety, behavioural disorder; multiple sclerosis; myathenia gravis;
maxiety, behavioural disorder; multiple sclerosis; myathenia gravis;
Whereast cancer allergy, addiction, asthma; transplantation;
Gravit versus host disease; systemic lupus erythematosus; scleroderma;
Graft versus host disease; systemic lupus erythematosus; scleroderma;
Whereast cohn's disease; HYY infection; human immunodeficiency virus;
we therosclerosis; cirrhosis; rhewmatoid arthritis; diabetes; pancreatitis;
Whereast propertial bleeding disorder; mischolar acidosis; skin disorder;
Whosporatic kidney disease, remal tubular acidosis; skin disorder;
Whematopoineric disorder; joint disorder; skeletal disorder;
Whematopoineric disorder; joint disorder; skeletal disorder;
Whosponadism; fertility disorder; viral infection; bacterial infection;
Whyosponadism; fertility disorder; viral infection; bacterial infection;
Whyosponadism; fertility disorder; viral infection; metabolic pathway modilation gene therapy;
Mical sodium/bile acid cotransporter; prohibitin MY: Clery spinessin;
macrophage stimulating procein precursor; fatty acid-binding protein;
Macrophage stimulating procein precursor; fatty acid-binding protein;
Macrophage stimulating procein; hepsin/plasma transmembrane serine protease.

WO200233087-A2.

25-APR-2002.

17-OCT-2000, 2000US-241063P.
20-OCT-2000, 2000US-241543P.
21-OCT-2000, 2000US-242482P.
23-OCT-2000, 2000US-242482P.
23-OCT-2000, 2000US-242482P.
23-OCT-2000, 2000US-242880P.
24-OCT-2000, 2000US-242880P.
24-OCT-2000, 2000US-242880P.
25-ARR-2001, 2001US-245903R.
25-ARR-2001, 2001US-245903R.
25-ARR-2001, 2001US-245903R.
25-ARR-2001, 2001US-245903R.
25-ARR-2001, 2001US-245903R. 17-OCT-2001; 2001WO-US32496

(CURA-) CURAGEN CORP.

Edinger S, Gerlach V, MacCougall JR, Malyankar UM, Smithson G; Millet I, Peyman JA, Stone DJ, Gunther E, Ellerman K, Shlankets RA; Padigaru M, Guo X, Patturajan M, Taupier RJ, Burgess CE; Zertusen BD, Kekuda R, Spytek KA, Gangolli EA, Fernandes ER;

WPI; 2002-590434/63. N-PSDB; ABS59324. Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nuclear acide mercing the polypeptides for diagnosing and treating nuclear acide mercing the polypeptides for diagnosing and treating e.g. cancer, Althemer's disease, cardiomyopathy, metabolic disease and e.g. cancer, Althemer's disease, cardiomyopathy, metabolic disease and diabetes

Claim 1; Page 15; 305pp; English.

The present invention relates to new NOVY (NOVI-10) polypeptides. The molecules of the invention are useful for treating or preventing a NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, or NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, or disorder related to cell signal processing and metabolic pathway modulation in humans. NOVX polypeptides, nucleic acids and antibodies are useful for treating or preventing disorders or syndromes including care useful for treating or preventing disorders or syndromes including care useful for treating or preventing disorders or syndromes including care useful for treating of sease, publication as disease, anxiety, behavioural disorders, multiple sclerosis, mysthenia gravis, anxiety, behavioural disorders, multiple sclerosis, mysthenia gravis, chiesase, allergies, addiction, asthma, endometriosis, graft versus host disease, allergies, addiction, asthma, endometriosis, graft versus host chemoscorpenia, chiencae, intendant immunodeficiency virus) infection, thermoscorpenia, chiencae, intendant since artherosclerosis, chience disorders, remarkable in disorders, congenital diarrhoea, respiratory disease, gastro-intestinal disorders, congenital distribers, obtains and skeletal disorders, muscle bone, joint and skeletal disorders, dental disease, and infection, growth and reproductive disorders, whopognadiem, fertility, and/or other the present amino acid sequence represents a NOVX protein of the

791 AA; Sequence

7; Indels 163; Gaps 78.4%; Score 4103.5; DB 23; Length 791; 81.2%; Pred. No. 0; tive 9; Mismatches 7; Indels 163; Local Similarity 81.2 1es 774; Conservative Query Match Matches

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61 PLFSAGTCVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ 120

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                                                                                                                                                                                                                                               352 LLRSHRNEELNVETLVVVDXKAMQNHGHENITTYVLTILNMVSALFKDGTIG-----403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 ALLLTGLDICSWKNEPCDTLGFRPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMI 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480 HDGEGNMCKKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYK 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 SACTIHRGLYTKHHHTN-YYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWT 678
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PLFSAGTCVRHGTRSGSAMEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQCTNTGTENQ 120
                                                                                                                                                                                                                                                                                                            300 SLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRS 359
                                                                                                                                                                                                                                                                                                                                  301 SLSNKVKDGTPCSEDSRNVCIDGICE------MPQPPKEDLFILPDSYKSCLRHKRS 351
                                                                                                                                                                                                                                                                                                                                                                                          360 LLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKOGLMGKDGTRHDH 419
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                                                               TLHVLT-OYDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMD
                                                                                                                                             180 LRTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRT
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The invention relates to a polypeptide belonging to the ADAWTS family is selected from sequences appearing as AAU79496, AAU79497 and AAU79499, calcated from sequences appearing as AAU79496. But AAU79499, calcated for macking bolypeptide, a protein having not less than polypeptide, become and to polypeptide modified from any of the polypeptides but with some anno acids deleted, substituted, added or inserted Also included are the polypeptide modifieds encoding the polypeptides (or their complementary strands or variants). The polypeptide is transforment or polypeptide protein or polypeptide, protein or polypeptide, protein or polypeptide, protein or peptide and screening compounds to promote or inhibit expression of the polypeptide or protein or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, protein, protein or polymulectide by using the polypeptide protein, protein, protein or polymulectide by using the polypeptide protein, protein, protein or the presence of a test compound for connect before evaluating the colymulectide by using the polypeptide protein, protein, protein or the presence of a test compound for connect before evaluating the activity by measuring adaposis and screening compounds for dway composition are applicable in dagnosis and screening compounds for way composition. The gene encoding such polypeptide may any including gene thrapy.

The gene encoding such polypeptide has conserved reprolycia-type zwing and post-operative healing failure, including gene thrapy.

The gene encoding such polypeptide has conserved reprolycia-type zwing and control protein of the polypeptide and docation of the gene on the 5P-syndrome delation site on thromosome 5p15.2-15.3 (associated with
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refractory skin ulcer; gastric ulcer; post-operative healing failure; reprojyshi-type 2N-metalloprofease domain; disintegrin-like domain; TSP1; thrombospondin type 1 domain; saxual cycle; tumour; 5P-syndrome deletion; chromosome 5p5,2-15.3; Cri-du-chat syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain-originated ADAMTS family polypeptide and encoded gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%; Score 3858.5; DB 23; Length 1224; 75.6%; Pred. No. 3.1e-309; cive 24; Mismatches 72; Indels 143; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yasuda S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagase T, Nomura N, Yano K, Murakami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 146-150; 172pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                (KAZU-) KAZUSA DNA RES INST FOUND.
(MITS-) MITSUBISHI PHARMA CORP.
                                                                                                                                                                                                                                                                          11-OCT-2001; 2001WO-JP08913.
                                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000JP-0311309.
02-APR-2001; 2001JP-0102905.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABK49822.
                                                                                                                                                                            WO200231163-A1.
                                                                                                                               Homo sapiens.
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vasotropic; antimigraîne, analgesto; endocrine; nocropic; tranquiliser, hypertesive, hypotensive, neuroleptic; neuropicitie; nabolic; anorectic; antimiflamatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; heematopoietic; breast; colon; lung, prostrate; cervical; brain, ovarian; bladder; kidney; pain; immune=related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder;

Caenepeel S;

Plowman GD, Whyte D, Sudarsanam S, Manning G,

(SUGE-) SUGEN INC.

WPI; 2002-041502/05.

Payne V;

N-PSDB; AAS97174

04-MAY-2001; 2001WO-US14431. 04-MAY-2000; 2000US-201879P.

WO200183782-A2. Homo sapiens.

08-NOV-2001.

Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;

4	20 CK	S	œ
3	3)
λò	121 TL	LHVLTQYDLVSAXEVDHRGDYVSHEIMHQRRRRAVAVSEVESLHIRLKGPRHDFHMDL 18	80
qc qc	65	SLHLRLKGPRHDFHMDL	112
à	81.39	TESSIVARGETVQTLGKTGTKSVQTLPPEDFCFYQSSLRSHRNSPSHGGRFCEGSTRTL 2:	240
qq	m m	RSHRNS-SVALSTCQGLSGMI	171
à	241 KL	HYKWKPYTQVEA-DLCKLYCI 2	91
qc	172 R-	RTEEADYFLRPLPSHLSWKL-GRAAQGSSPSHVLYKRSTEPHAPGASEVLVT 2:	22
λ;	292 AE	GFOFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHNPQPPKEDLFILBDE 3	49
q	223 SF	23 SRIWELAHQPLHSSDLRLGLPGRRKKYMPQPPKEDLFILPDE 27(10
'n	350 YR	SCLRHKRSLLRSHRNEELNVETLVVVDKKMQNHGHENITTYVLTILNMVSALFKD 4	0.7
q	271 YR	:SCLRHKRSLLRSHRNBELNVETLVVVDKKAMQNHGHENITTYVLTILNMVSALFKDGT 3:	30
ć	408	GLMGKDGTRHDHAILLIGH	27
QQ	331 IC	GONINIAIVGLILLEDEQPGLVISHHADHTLSSFCQWQSGLWGKDGTRHDHAILLTGLD 39	90
ò	Η-	4	87
ପ୍ପ	91 I	CSWKNEPCDILGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 4	20
δý	488 K	KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGE 5-	47
do	451 K	S	10
ò	548 L	w	10.3
qq	511	ď	04:
ò	608 GC	GGQCVKYGDEGPKPTHGHMSDWSSWSPCSRTCGGGVSHKSRLCTNPKPSHGGKFCEGSTR 6	199
qq	ä	CEGSTR 6	30
<i>λ</i> ο	œ	AEGFOF 7	127
qq	631 TI	TLKICNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVBDQDLCKLYCIAEGFDF 6:	06:
٥٨	728 FI	7	187
ą,	m	7	.50
ò	788 [1]	LYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHMTVDWPGRYK 8	347
QQ Q	751 [7]	w	81.0
ò	848 FS		204
qq	811 5		870
λō	808	YTWAIVRSECSVSCGGGR 926	
qa	871 \$		

13; S (Which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, coprition disorders in proteinsion, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or protease anino acid sequences of the invention. 121 TLHVLTQYDLVSAYEVDHRGDYVSHEIMHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL 180 181 RTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL 240 61 PLFSAGTCVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDBAGNHRSQQTNTGTENQ 120 59 -----EYDLVSAYEVDHRGDYVSHEIMHHQRRRAVAVSEVESLHLRLKGPRHDFHMDL 112 113 RTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNS-SVALSTCQGLSGMI 171 The invantion relates to an isolated, enriched, or purified procease polypeptide (1) and polynucleoride (11) encoding (1). (1) may be used to screen for substances (5) that may modulate its activity. Administering 1 MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRKLTAMS 60 1 MKPRARGWRGLAALWMLLAQVAEQAP------ACAMG 31 72; Indels 143; Gaps 32 PAAAA-----PGSPSVPRPPPPABRPG------WMEKG-----Claim 28; Figure 2D; 232pp; English. 1224 AA; disorders Sequence

Novel processe polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, e.g., cancers, immune-related diseases. Ouery Match 73.7%; Score 3858.5; DB 23; Length 1224; Best Local Similarity 75.6%; Pred No. 3.1e.309; Macches 740; Conservative 24; Mismatches 72; Indele 143; C ઠે 요 à 뭐 ò g ò

Human metalloprotease partial protein seguence #3.

(first entry)

AAU72891 standard; Protein; 1224 AA.

AAU72891

AAU72891;

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608 GGQCVKYGDEGPKPTHGHMSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGSTR 667
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                       R-----TEEADYFLRPLPSHLSWKL-GRAAQGSSPSHVLYKRSTEPHAPGASEVLVT 222
                                                                                                350 YKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILMWVSALFKD-- 407
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241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKWKPYTQVBA-DLCKLYCI 291
                                                                                                                                                                                                                                                                                                                      LYDANIOCKWQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKFMPAAEGTICGHDMMCR
                                               292 AEGFDFFFS--LSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
                                                               KKSEGNIMSPTLAGRNGVFSWSPCSROYLHKFLSTAQAICLADQPKPVKEYKYPBKLPGE
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transforming growth factor-beta inhibitor, chronic renal failure.
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MDTS9 procease. The MDTS9 DNA and procein sequences of the invention are useful for screening for transforming growth factor (TGF)-beta inhibitors and for the treatment of chronic renal failure. The present amino acid sequence represents the human MDTS9 procease of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR------HYKWKPYTQVEA-DLCKLYCI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 YKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKD-- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GLMGKDGTRHDHAILLIGLD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 IGGNINIAIVGLILLEDEQPGLVISHHADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS 60
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequence of the human
                                                                                                                                                                                                                                                                                           Protease MDTS9 and encoded polynucleotide, applicable in diagnosis and screening TGF-beta inhibitors for treatment of chronic renal failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AEGFDFFFS--LSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 PAAAA-----PGSPSVPRPPPPAERPG------WMEKG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 ICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels 143; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 1224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKPRARGWRGLAALWMLLAQVAEQAP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.5%; Score 3846.5; DB Best Local Similarity 75.4%; Pred. No. 3e-308; Matches 738; Conservative 25; Mismatches 7.
                                                                                                                                                         Ogino M;
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 48-51; 60pp; Japanese.
                                                                                                                                                         Abe K,
                                                                                                       (YAMA ) YAMANOUCHI PHARM CO LID
                                                  25-DEC-2000; 2000JP-0393372.
21-DEC-2001; 2001WO-JP11251
                                                                                                                                                            Yamaji N, Nishimura K,
                                                                                                                                                                                                                  WPI; 2002-508888/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1224 AA;
                                                                                                                                                                                                                                         N-PSDB; AAL43654
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547

13;

Ov 1 MKPRAROWRGLAALAWILLAOVAEOVSPCRSHORGNRGSGOLEASPPRLLSRGPFRLTAMS 60		32	59EYDLVSAXEVDHRODYVSHEIMHQRRRRAVASSEVESLHLRLKGSRHDFHVDL	181 RISSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFVQGSLRSHRNSPSHGGKFCEGSTRTL	DD 1.3 KISSSLVARGRIVQILGKKIGIKSVQTLAREDECRYQGSLASHKNS-SVALSTCQSLSGMI 171 Qy 241 KLCNSQXCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEA-DLCKLYCI 291	bb 172 RTBEADYPI.RPI.PSHLSWKL-GRAAQCSSPSHVI.YKRSTBPHAPGASEVI.VT 222	292 AEGFDFFSLSNKVKDCTPCSEDSRNVCIDGICELSVVSTSAHMPQPEKEDLFILPDE ::	223 SRTWELAHQPLHSSDLRLGLPQKQHFCGRRKKYMFQPFKEDLF1LFDE 350 YKSCLRHKRSLLRSHRBELAVETLUVVDKROMQNHGHENITTYVLTILMMVSALFKD	Db 271 YKSCLRHKRSLLRSHRNEELNVFTLVVVDKKMMQNHGHENITTVVLTILNMVSALFKDGT 330	408GLMGKDGTRHDHAILLITGLD	331 IGGNINIAIVGLILLEDEQPGLVISHHADHTLSSFCQRQSGLMGKDGTRHDHAILLTGLD	Oy 428 ICSWKNEPCDTLGFAPISGWCSKYRSCTINEDTGLGLAFITAHESGHNFGMIHDGEGNWC 487 191	1971 ICOMANDE COLLGRAFTOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	(y) 488 KUSEGAIMSTTAGENGVESMECKROTAKELSTAGAICLADORKPYKEKYPEKLEGE 547 [1] [[] [[] [] [] [] [] [] [] [] [] [] []	יייי בייייניין אין אין אין אין אין אין אין אין אין	OY 548 LYDANIQCKROPOBIAKLOVLDFKKDITCKALMCHRISTRKCETKRNPALAGTITCHDWNCR 607 D) 511 [ANDANIOCKROPOBIAKATIONIDEKROTOKALWCHRISTICH FILL	STATE OF CHARGE STATE OF THE CONTROL	S71 GOOCKYCOBEOPEPHACHASIAS POSTUCACACINES PROCESS PRO	668 TIXICNSOKCPRESUDERAACARHNSRERGRHVWWKEVTOVEDODICKIAEGEDE	631 TLKLCNSQKCPRDSVDFPRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDF	Qy 728 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVGGVCNGNNSACTIHRG 187	Qy 788 LYTKHHHTNQYYHNVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYK 847	Db 751 LYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWFVDWFGRYK 010	Qy 848 FSCTTPDYRRSYNEPRILIATOPINETLIVELLFQGRNPGVAMPYSNPRICTEXQPPAQP 907	DD 811 FSGTTFDYRRSYNEPENLIATGFINETLIVELLFQGRNPGVAMPRYGMPRLGTBKQPPAQP 870	Qy 908 SYTWALVRSECSVSCGGR 926	Db 871 SYTWAIVRSECSVSCGGQ 889	RESULT 8 AAU80153 ID AAU80153 standard; Protein; 1224 AA.
Db 571 GGCCVKYGDEGPKZTHGHWEDWSGWSPCSRTCGGCVSHRSKLCTNPRPSHGKKCEGSTR 630	668 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRPRGRHYKWRPYTQVEDQDLCKLYCIAEGPDF 	QY 728 PFSLSNKVKDGTPCSEDSRNVCIDGICERVQCDNVLGSDAVEDVČQVCNGNKSACTIHKG 787 DA 6.91 PPGLSNVKRCGTPCSEDSRNVCTTCPRVGCDNVLGSDAVEDVCGVCNCSNSCACTIBG 750	788 LYTKHHHTMQYYHMVIIPSGARSIRIYEBMYSTSYISVRNALRRYYLMGHMTVDBACRYK	751 LYTKHHINQYYHMVI I PSGARSIR LYBNIVGESIVSNALARXYLMGHINTII II II II II II II II II II II II II	OV 848 FOLITEURINDERINDERINGENEUR FOR THE PROPERTY OF THE PROP	Qy 908 SYTWAIUNSECSUSGGGR 926	Db 871 SYTWAIVRSECSVSCGGGQ 889	REGULT 7 ABG72431 ID ABG72431 standard; Protein; 1224 AA.	XX AC ABG72431;	XX DT 05-FE8-2003 (first entry)	XX DE Novel human protease #2.	XX XW Human; protease; gene therapy; obesity; enzyme. XX	OS Homo sapiens.	AAA USG448388-B1. XX XX	PD 10-SEP-2002.	AAA 15-AUG-2001; 2001US-0930872 XX	PR 16-AUG-2000; 2000US-225852P. XX	XI-) LEXIC	PI Friddle CJ, Hilbun E; XX	DR WPI, 2003-074103/07. DR N-PSDB, ABSS7767, ABSS7768.	New nucleic acid encoding novel human protein (NHP), useful for the PT preparation of a medicament for diagnosing, preventing or treating PT disorders or diseases associated with the NHP, e.g., obesity	im 4; Column 19-26; 17pp; English.	XX XX The invention describes a new isolated nucleic acid comprising a	c. sequence that encodes a fully defined protein sequence comprising 491 CC or 1224 amino acids or that hybridises under stringent conditions with CC the 3475-bb sequence or its complement. The muchet acid is useful for	CC the preparation of a medicament for diagnosing, preventing or treating CC disorders (e.g. using done therapy) or diseases associated with the	CC novel human proteins, e.g., obesity. This sequence encodes a novel	XX SQ Sequence 1224 AA;	Query Match 73.5%; Score 3846.5; DB 24; Length 1224; Best Local Similarity 75.4%; Pred, No. 3e-308; Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;

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Human, ADANTS; cytostatic; antidiabetic; antirheumatic; antiathritic; antialcer; vulnerary; neovascularisation; angiona; antialcer; vulnerary; neovascularisation; angiona; diabetic omentopathy; chronic rheumatoid arthritis; gene therapy; refractory skin ulcer; gastric ulcer; post-operative healing failure; regerolysin-type 2N-metallopycease domain; disintegrin-like domain; TSP1; thrombospondin type 1 domain; sexual cycle; tumour; SP-syndrome deletion; chromosome 5p15.2-15.3; Cri-du-chat syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain-originated ADAWTS family polypeptide and encoded gene, applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nomura N, Yano K, Murakami K, Yasuda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Wild-type Met substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild-type Ser substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Wild-type Pro substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page -; 172pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAZU-) KAZUSA DNA RES INST FOUND. (MITS-) MITSUBISHI PHARMA CORP.
                                                                                                                                   Human ADAMTS protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2000; 2000JP-0311309.
02-APR-2001; 2001JP-0102905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001; 2001WO-JP08913.
                                                               15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         API; 2002-372277/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2002
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AAU80153;
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Human brain-originated ADAMYS family polypeptide and encoded gene, applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation ...

Example 2; Page -; 172pp; Japanese.

Example 2; Page -; 172pp; Japanese.

The invention relates to a polypeptide belonging to the ADAWYS family is celected from sequences appearing as ADAY9496, ADAY9497 and ADAY9499.

So homology with the amino acid sequence of the polypeptides or a polypeptide from any of the polypeptides by the sequence of the polypeptide or a polypeptide from any of the polypeptides by the sequence of the polypeptides or a polypeptides encoding the polypeptides by the second or variants), a recombinate vector containing any of the polypeptides encoding the polypeptide for transformant and inhibit activity of the polypeptide or protein or peptide and encoded sene transformant, an antibody that can recognize the polypeptide, protein or peptide or protein, or to promote or inhibit activity of the polypeptide or protein, or to promote or inhibit activity of the polypeptide, weetor, transformant or ontain the presence of a test compounds for contact before evaluating the polypeptide, by protein, peptide, weetor, transformant or contact before evaluating the activity by measuring signal changes. The polypeptide and encoded gene are applicable in diagnosis and screening compounds for drug composition; in the area propertied architics, and one neovascularisation, diabetic commentopathy; and paper presence of a test compound for contact before evaluating the area applicable in diagnosis, and screening compounds for drug composition; in the applicable in diagnosis, and screening compounds for drug composition, are applicable in diagnosis, and screening compounds to contact before evaluating the menaling failure, including gene therapy of the performance of a test composition, the performance of a test compounds to menaling failure, in contact performance of a test compounds to the performance of a test compound

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The invention relates to a polypeptide belonging to the ADAMTS family is selected from sequences appearing as AAMT9996, AMT9997 and AAMT9999.

So selected from sequences appearing as AAMT9996, AMT9997 and AAMT9999.

So knowledgy with the amino acid sequence of the polypeptides or a polypeptide modified from any of the polypeptides but with some amino acid selected, substituted, added or inserted. Also included are the polypeptides encoding the polypeptides (or their complementary polymucleotides encoding the polypeptides (or their complementary exercit producing the polypeptides (or their complementary term) and acreening or a transformat which is transformed with the recombinant vector. producing the polypeptide, protein or peptide by culturing the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the complymented of test compound for contact before evaluating the activity by measuring slighal changes. The polypeptide and encoded gene activity by measuring slighal complements of inhibit expression of the presence of a test compound for contact before evaluating the activity by measuring slighal complements or protein. The presence of a test compound for contact before evaluating the activity by measuring slighal complements or are applicable in diagnosis and screening compounds for drug compositions in the protein or protein or protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic rheumatoid arthritis, angioma, refractory skin and gastric ulcers and post-operative healing failure, including gene therapy.

The gene encoding such polypeptide has conserved reprolysin-type ZN-metalloprotease domain, disincegrin-like domain and TSP1 (thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ADANTS; cytostatic; antidiabetic; antirheumatic; antianceriation; angiona; antiancer; vulnerary; neovascularisation; angiona; diabetic ometropathy; orbonic rheumatoid arthritis; gene therapy; refractory skin ulcer; gastric ulcer; post-operative healing failure; reprolysin-type RN-metalloprocease domain; disintegrin-like domain; TSP1; thrombospondin type 1 domain; sexual cycle; tumour; SP-syndrome deletion; chromosome 5p15.2-15.3; cri-du-chat syndrome.
811 FSCTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAWEYSMPRLGTEKQPPAQP 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain-originated ADAWTS family polypeptide and encoded gene, applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
                                                                                                                                                                                                                            AAU79500 standard; Protein; 1170 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAZU-) KAZUSA DNA RES INST FOUND.
                                                    SYTWAIVRSECSVSCGGGR 926
                                                                                (MITS-) MITSUBISHI PHARMA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2000; 2000JP-0311309
02-APR-2001; 2001JP-0102905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001; 2001WO-JP08913
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Human ADAMTS protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-372277/40.
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                                                                                                                                                                                                                                                                           AAU79500;
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                                                    906
                                                                                                   871
                                                                                                                                                                                                      AAU79500
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                                                                                                                                                                                                                                                                                                          127 QYDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VAPGFIVOTLGKTGTKSVOTLPPEDPCFYQGSLRSHRNS-SVALSTCQGLSGMIR---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 ---TEEADYFLRPLPSHLSWKL-GRAAQGSSPSHVLYKRSTEPHAPGASEVLVTSRTWEL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 FFS--LSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 AHQPLHSSDLRLGLP---QKQHFC-----GRRKKYMPQPPKEDLFILPDBYKSCLR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 HKRSLLRSHRNBELNVETLVVVDXKAMQNHGHBNITTYVLTILNMVSALFKD----- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 HKRSLLRYHRNEELNVETLVVVDKKMAQNHGHENITTYVLTILNMVSALFKDGTIGGNIN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGN 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 YGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGGSTRTLKLCN 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSN 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 KVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHH 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTNOXYHMVTIPSGARSIRIYEMNVSTSVISVRNALRRYYLNGHWTVDWPGRYKFSGTTF 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAWEYSMPRIGTEKQPPAQPSYTWAI 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYRRSYNEPBNLIATGPINETLIVELLFQGRNPGVAMEYSMPRIGTEKQPPAQPSYTWAI 822
                                                                                                                                                                                                                                                                                                                                                                                                      187 VAPGFIVQTLGKTGTKSVQTLPPEOFCFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNSQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 KCPRDSVDFRAAQCABHNSRRFRGR-----HYKWKPYTQVBA-DLCKLYCIAEGFDF 297
                                                                                                                                                                                                                                                                                                                                       SILILIA SAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGSRHDFHVDLRTSSSL 64
type 1) domain. Its encoded protein is characterised by high expression in ovaries, changes in expression dose depending on the sexual cycle, a decrease in tumour cell and location of the gene on the 5P-syndrome delation site on chromosome 5p15.2-15.3 (associated with cri-du-chat syndrome). The present sequence represents a ADMYTS protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GLMGKDGTRHDHAILLTGLDICSWKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 IAIVGLILLEDEQPGLVISHHADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLDICSWKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 EPCDILGFAPISGMCSKYRSCTINEDIGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGN
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                                                                                                                                                                                                                                                                 75; Gaps
                                                                                                                                                                                                             71.6%; Score 3750.5; DB 23; Length 1170; 82.3%; Pred. No. 2.4e-300; tive 23; Mismatches 53; Indels 75;
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Best Local Similarity
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Whuman, NOVX; cardiomyopathy; atherosclerosis; cell signal processing; breast cancer, Altaheimer's diesease; peliplesy; Huntington's disease; an exast cancer, Altaheimer's diesease; pain; stroke; adsance; according autocommune diesease; altergy; addiction; asthma; transplantation; autocommune diesease; altergy; addiction; asthma; transplantation; autocommune diesease; altergy; addiction; asthma; transplantation; system contrasts; cronn's diesease; systemic lupus crythematosus; scleroderma; psortiasis; cronn's diesease; theumatoid arthritis; diabetes; pancreatitis; which compocytopenia; breading diseorder; metholic disorder; obseivy; glucose transport defect; glomerulonephritis; hypercalicemia; please; reapliatory disease; satio-intestinal disease; maccle disorder; bone disorder; point disorder; skeletal disorder; hadmatopolatic disorder; point disorder; posteoprovisis; hadmatopolatic disorder; point disorder; reproductive disorder; hypogonadism fettility disorder; viral infection; becterial infection; paralle, processing since therapy; and metabolic pathway modulation; gene therapy; although a sodium beta-5 protein; reprohibitin; gene therapy; incleation and processing protein; prohibitin; gene therapy; since metalloprocease; and contamporter; prohibitin; WT; CTP, sphinding protein; where and processing protein; protein; protein; protein; protein; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; since metalloprocease; pathway modulation; gene therapy; specially since pathway modulation;
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                                                                       ABG76896 standard, Protein, 856 AA.
                                                                                                                                                                                                                                                                                    Human ADAM-TS 7-like protein #1.
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2001US-303698P.
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Zerhusen BD,
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29-MAY-2001;
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Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheimer's disease, cardiomyopathy, metabolic disease and diabbees

The present invention relates to new NOVX (NOV1-10) polypeptides. The molecules of the invention are useful for treating or preventing a novicule disorder, such as cardiomyopathy, atherosclerosis, or NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, or NOVX-associated disorder, such as cardiomyopathy, atherosclerosis, or disorder related to cell signal processing and metabolic pathway modulation in humans. NOVX bolypeptides, mucleic acids and antibodies are useful for treating or preventing disorders or syndromes including breast center, behavioural disorders, multiple scherosis myasthemia gravis, anxiety, behavioural disorders, multiple scherosis, myasthemia gravis, anxiety, behavioural disorders, multiple scherosis, graft versus host disease, altergies, addiction, aschima, endometriosis, graft versus host disease, altergies, addiction, aschima, endometriosis, graft versus host caseas, systemic lupus erythematosus, scleroderma, transplantation, psoriasis, crohn's disease, HIV (human immunodeficiency virus) infection, thrombocytopenia, bleeding disease, matched, glomexuloneparities, hypercalcremia, polycystic glucose transport defect, glomexuloneparities, hypercalcremia, polycystic glucose transport defect, glomexuloneparities, congenital disarchesa, repairatory disease, gastro-intestinal diseases, congenital disarchesa, repairatory disease, gastro-intestinal diseases, unimary system disorders, osteoporosis, dental diseases and infection, cumacle, hoom, joint and skelteal disorders, mancele, hoom, goint and skelteal disorders, extra report and disorders, viral, bacterial, or parasitic infections. The present amino acid sequence represents a NOVX protein of the 16; 129 DLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGRRHDFHMDLRTSSSLVA 188 455 430 76 NSOPGFLNLSNVRSHWREQHASKRIITNAMLGESALASTRKSNCVFFLSFYFFQSGMIRT 135 22 H-----RNSPSH----GGKFCEGS------TRTLKLCNSQKCPRDSVDFRA 257 136 EEADYPLRPLPSHLSWKLGRAAQSSPSHVLYKREVLVTSRTWELAHQ---PLHSSDLRL 192 258 AQCAEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTFCSEDSRN 317 318 VCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVV 377 456 INEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAGRNGVFSWSPCSRQY 515 576 KALWCHRIGRKCETKEMPAAEGTICGHDMWCRGGQCVXYGDEGPKPTHGHWSDWSSWSPC 635 22 19 DLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVEPAFLQVCRAR---ELRLCVEAFPIA 189 ---PGFI------FCFYQ-GSLRS 207 -----YMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVV -----GLMGKDGTRHDHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRSCT 311 DHTLSSFCQWQSGLMGKDGTRHDHALILLTGLDICSWKNEPCDTLGFAPISGMCSKYRSCT 371 INEDIGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAGRNGVFSWSPCSRQY 516 LHKFLSTAQAICLADQPKPVKBYKYPBKLPGELYDANTQCKWQPGEKAKLCMLDFKKDIC Query Match 64.3%; Score 3365; DB 23; Length 856; Best Local Similarity 71.9%; Pred. No. 1.1e-268; Matches 660; Conservative 25; Mismatches 59; Indels 174; Gaps 193 GL---PQKQHFCGRRKK------Claim 1, Page 18; 305pp; English. 856 AA; invention. Sequence 408 à à ద ò 쉺 ò 윱 à 음 à 셤 à 셤 ð 셤 ö 셤 ö

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instructions response to the protein sequences of the investing a compound for effectiveness as an another to a return transcribed by the protein sequences of the invention are useful for screening a compound for effectiveness as an another to a readoust the identified agonist and antagonist are useful for treating a disease or condition associated with decreased or overexpression of functional PRTS in a patient.

The PRTS protein is also useful as an immunogen for preparing polyclonal or monoclonal antibodies by hybridoma technology. An antibody that binds or he PRTS proteins is useful for detection and purification of the proteins and can be used to disgnose a condition or disease associated with expression of PRTS in a subject or in a biological sample. The proteins and can be used to disgnose a condition or disease associated with expression of partointestinal disorders such as gastritis, ulcerative of partointestinal disorders such as atherosclerosis, hypertension, myozardial infarction, etc. autoimmune/inflammatory disorders such as acquired immunodeficiency syndrome (AIDS), asthma, drawers and as acquired immunodeficiency syndrome (AIDS), asthma, heaving a portials, portials disorders such as dermatitis, scabies, communical disorders such as dermatitis, scabies, communical control of a partoin of the parton of the parton of the production of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provision of the provisio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dementia, Alzheimer's disease, Huntington's disease, multiple sclerosis, etc; or reproductive disorders such as infertility, impotence. The present sequence represents the PRTS4 protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568 MPAAEGTICGHDMWCRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCT
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     New human protesses useful for diagnosing, preventing or treating anorexis, myocardial infarction, Addison's disease, hepatitis, Cushing's syndrome, eczema, Parkinson's disease, and impotence
                                                                                                                                 DNA and protein sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.8%; Score 3286; DB 23; Pet Local Similarity 93.1%; Pred. No. 6.1e-262; Matches 591; Conservative 2; Mismatches 0;
                                                                                        Claim 1; Page 135-137; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTILNMVSALFKD-----
                                                                                                                                 This invention relates to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ulcerative colitis; Reye's syndiome; cardiovascular disorder; enzyme; hypertension, mycardial infarction; autoimmune disease, AlbS, PRTS; inflammatory disorder; acquired immunodeficiency syndrome; asthma; Grave's disease, cell proliferative disorder; hepatitis; psoriasis; leukaemia; developmental disorder; Cushing's syndrome; impotence; epithelial disorder; Cushing's syndrome; impotence; epithelial disorder; dementials disorder; dermatitis; scabies; ecrema; neurological disorder; Huntingon's disease, dementia, Albreimer's disease, infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease; human; gastrointestinal disorder; gastritis; atherosclerosis;
                    RRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGIC
                                                                                                     RRFRGRHYKWKR-----DQDLCKLYCIAEGFPFFFSLSNKVKDGTPCSEDSRNVCIDGIC
                                                                                                                                                                                                                                                                           SRICGGGVSHRSR-LCINPKPSHGGKFCEGSTRILKLCNSOKCPRDSVDFRAAQCAEHNS
                                                                                                                                                                                                                                                                                                                                      LIVELLFQGRNPGVAWEYSMPRLGTEKQPPAQPSYTWAIVRSECSVSCGGRCLPVLLLE
                                                                                                                                                                                                                                                 EMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKRSGTTFDYRRSYNEPENLIATGPTNET
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A, Lu DAM, Baughn MR, Delegeane AM, Burford N,
Lee S, Xu Y, Griffin JA, Kallick PA, Gandhi AR;
Ison CH, Tang YT, Azimzai Y, Eliliote VS, Swarnakar A;
J, Nguyen DB, Tribouley CM, Lo TP, Au-young J;
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2-CCT-2000; 2000US-24543P.
02-NOV-2000; 2000US-245256P.
15-NOV-2000; 2000US-24835F.
16-NOV-2000; 2000US-248326P.
20-NOV-2000; 2000US-248326P.
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Borowsky ML, Lee S, Xu Y,
Arvizu C, Ison CH, Tang Y
Ramkumar J, Nguyen DB, Tr
Thangavelu K, Kearney L;
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N-PSDB; ABK86137.
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The invention relates to a polypeptide belonging to the ADAWTS family is selected from sequences appearing as ANJO $465. MAJO $497 and ANJO $499.

Selected from sequences appearing as ANJO $465. MAJO $497 and ANJO $499.

The sequences appearing a protein having not less than a protein that contains the polypeptide, a protein having not less than 50 yeaptoptide modified from any of the polypeptides but with some amino acid sequence of the polypeptides of acids delated, substituted, added or inserted. Also included are the polypeptides encoding the polypeptides (or their complementary strands or variants), a recombinant vector containing any of the polypeptide, protein or producing the polypeptide, protein or peptide and screening compounds to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide or protein, or to promote or inhibit expression of the polypeptide by presence of a test compound for contact before evaluating the activity by measuring signal changes. The polypeptide and encoded generative plantand diseases and ecreening compounds for drug compositions in the presence of a test compound for contact before evaluating the activity by measuring signal changes. The polypeptide and encoded generative are applicable in diagnosis and screening compounds for drug compositions in treating diseases and the polypeptide and encoded generative healing failure, including gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarthritic; antiulder; vulnerary; neovascularisation; angioma; diabetic omentopathy; chronic rheumatoid arthritis; gene therapy; refractory skin ulcer; gestric ulcer; post-operative healing failure; reprolysin-type ZN-metalloprocease domain; disintegrin-like domain; TSP1; thrombospondin type I domain; sexual oyole; rumour; SP-syndrome deletion; chromosome Spis,2-15.3, C11-du-chet syndrome.
Human brain-originated ADAWTS family polypeptide and encoded gene, applicable in diagnosis and screening compounds for drug compositions in treating diseases due to e.g. neovascularisation
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ADAMTS; cytostatic; antidiabetic; antirheumatic;
                                                                                              868 YSMPRIGTEKQPPAQPSYTWAIVRSECSVSCGGGG 902
                                                                    892 YSMPRLGTEKQPPAQPSYTWAIVRSECSVSCGGGR 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 123-127; 172pp; Japanese.
                                                                                                                                                                                                                                    AAU79496 standard; Protein; 1021 AA.
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(MITS-) MITSUBISHI PHARMA CORP.
                                                                                                                                                                                                                                                                                                                                                                              Human partial ADAMTS protein #1.
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02-APR-2001; 2001JP-0102905.
                                                                                                                                                                                                                                                                                                                                      (first entry)
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DODLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICBRVGCDNVLGSDAVEDV 771
                                                                                                                                                                                                                                                                                                                               52 YMPQPPKEDLFILFDEYKSCLRHKRSLLRYHRNEELNVETLVVVDKKWMQNHGHBNITTY 111
                                                                                                                                                                                                                                                                                                                                                                                      -----GLMG 411
                                                                                                                                                                                                                                                                                                                                                                                                                             112 VLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISHHADHTLSSFCQMQSGLMG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 KOGTRHDHALLTGLDICSWKONEPCDTLGFARJSGMCSKYRSCTINEDTGLGLAFTIAHE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 MPAAEGTICGHDMWCRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCT 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 MPAABGTICGHDMWCRGGGCVKYGDEGPXPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCT 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 CGVCNGNNSACTIHRGLYTKHHTNQYYHMYTIPSGARSIRIYEMVVSTSYISVRNALRR 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYLNGHWTVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTNBTLIVELLFQGRNPGVAWE 651
The gene encoding such polypeptide has conserved reprolysin-type ZN-metalloprotease domain, and TSD (thrombospondin type 1) domain. Its encoded protein is characterised by high expression in ovaries, changes in expression dose depending on the sexual cycle, a decrease in tumour cell and location of the gene on the 5P-syndrome deletion site on chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The present sequence represents a ADAMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAM TS-like finc meralloprotease; TNF antagonist; psychosis; bebantagonist; COPD, congestive heart fallure myocardial infarction; schaemic heart disease; arrhythmia; hypertension; vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 SGHNFGMIHDGEGNMCKKSEGNIMSPTLAGRNGVFSMSPCSRQYLHKFLSTAQAICLADQ
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                         334 HMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTY
                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                            62.6%; Score 3280; DB 23; Length 1021; 92.9%; Pred, No. 1.5e-261;
                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                             protein of the invention.
                                                                                                                                                                                                                                                                    Matches 590; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           394 VLTILNMVSALFKD-
                                                                                                                                                                                       1021 AA;
                                                                                                                                                                                                                                                  Local Similarity
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DSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTXHHHTNQYYHMVT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aggrecanase and encoded polynuclectide involved in causing joint diseases, applicable in screening inhibitors as preventives or remedies for treating the diseases e.g. osteoarthritis and rhoumatoid arthritis
GHWSDWSSWSPCSRTCGGGCVSHRSRLCTNPKPSHGGKFCEGSTRTLKLCNSQKCPRDSVD
                                                                                            FRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSE
                                                                                                                                                                                     FRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSE
                                                                                                                                                                                                                                                                    DSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMVT
                                                                                                                                                                                                                                                                                                                                1PSGARSIRIYEMNVSTSXISVRNALRRYXLNGHWTVDWPGRYKFSGTTFDYRRSYNEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, aggrecanase; MDTSB; enzyme; osteoarthritis; joint disease; metalloprocase and disintegrin with thrombospondin type 1 repeats; theumatoid arthritis; osteopathic; antitheumatkd; antiathritis; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human protein having aggrecanase activity, designated MOTS8 (metallopyrocease and disintegrin with thrombospondin type 1 repeats 8). The human MOTS8 protein has osteopathic, antirheumatic and antiarthritic activities. The human MOTS8 protein and polynoclacide are applicable in screening inhibitors as preventives or remedies for treating joint diseases in Steopathritis and rheumarcid arthritis. Human MOTS8 has been located to chromosome 16, and more specifically to chromosome 16, and more specifically to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human aggrecanase MDTS8 protein SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81460 standard; Protein; 1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel isolated polymucleotide encoding an CMAM-TS-like zinc metalloprotease polygeptide. The protein of the cardination may have cardinath, asotropic, antiarrhythmic, hypotensive, artiparkinsonian, noctropic, antiarrhythmic, hypotensive, artiparkinsonian, noctropic, neuroprotective, creatportective, cartiparkinsonian, noctropic, neuroprotective, creatportective, artiparkinsonian, noctropic, neuroperotective, creatportess, articonvulsant, anti-HIV neuroleptic and tranquiliser activity.

The DNA sequence of the invention may be used in gene therapy as a crime particular of the invention may be used in gene therapy as a carticonvollant state and comparison and expension which are alloproteases an expression vector containing the ADAM-TS-like zinc metalloprotease. These reagents can be used in the manufacture of a medicament for disorders such as Cropp, cardiovascular disease (congestive heart failure, myocardial infarction, isohaemic heart disease, atrial and ventricular arrhythmias, hypertension and peripheral vectors at a disease, and activated a schizophrenia, spychosis and attention of Creutzfeld-Jakob dementia, schizophrenia, spychosis and attention can also be used for screening and disponstition seave. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                  dementia, multiple sclerosis; stroke, Alzheimer's disease; dementia;
Huntington's disease; Creutzfeld-Jakob disease; dementia; schizophrenia;
attention deficit disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ISGMCSKYRSCTINEDIGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAGRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 KLCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTICGHDMWCRGGQCVKYGDEGPKPTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DEQPGLVISHHADHTLSSFCQWQSGLMGKDGTRHDHAILLIGLDICSWKNEPCDTLGFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAGRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide encoding an ADAW-TS-like zinc
retailoprocease polypeptide, useful for preventing, amelioxating or
treating dystunctions such as COPP. ONs and cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
     cerebrovascular disorder; Parkinson's disease; motor neuron disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2812.5; DB 23; Length 556;
Pred. No. 2.5e-223;
1; Mismatches 2; Indels 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 119pp; English.
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Matches 508; Conserv
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                                                                                                                                                        WO200257461-A2.
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ABJ19379 standard; Protein; 1162
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                                                                                      HEIMHHQRRRRAVAVSBVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSV
                                                                                                                                   OK-PEVQQCFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLPQ----LLA
                                                                                                                                                                                                                                        187 QEHNYSSPAG-HHPHVLYKRTAEEKIQRYRGYPG-----SGRNYPGYSPSHIPHASQS
                                                                                                                                                                                                                                                                                   239 RETEYHHRRLQKQHFC-----GRRKKYAPKPPTEDTYLRFDEYGSSGRPRRSAGKS
                                                                                                                                                                                                                                                                                                                               348 LEQEPGGLLINHHADQSLNSFCQWQSALIGKNGKRHDHAILLTGFDICSWKNEPCDTLGF
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                                                                                                                                                                     OTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNSO----KCPRDSVDFRAAQC
                                                                                                                                                                                                                     261 AEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDG-----TPCSEDS
                                                                                                                                                                                                                                                                    R-----NVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRS
                                                                                                                                                                                                                                                                                                                 364 HRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDG------
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                                                                                                                                                                                                                                                                                                                                                                  -----LMGKDGTRHDHAILLTGLDICSWKNEPCDTLGF
                                               Gaps
                      n 46.5%; Score 2435.5; DB 23; Length 1221;
Similarity 51.3%; Pred. No. 1.18-191;
66; Conservative 118; Mismatches 199; Indels 129;
                         Length 1221;
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1221 AA;
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protozoacide; neuroprotective; antiparkinsonian; antilipaemic; NOV.-associated disorder; decidolic disorder; metabolic disorder; disorder; ancreatis obesity, infectious disorder; ancer-associated cachexia; immune disorder; neurodegenexative disorder; Alzheimer; a disease; Parkinson's disease; haematopoietic disorder; cancer; disalpidaemia; metabolic disturbance; neurogenesis; call differentiation; call proliferation; haematopoiesis; wound healing; angiogenesis; gene therapy; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; NOVX.
                                                                                                                                                                                                                        nootropic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson DW, Zerhusen BD, Li L, Zhong M, Casman SJ, Gerlach VL; Shimkets RA, Gorman L, Pena CEA, Kekuda R, Patturajan M; Spytek KA, Leite MW, Sastell L, Macdougall JR, Taupier RJ, Guo Miller CE, Shenoy SG, Hjatt T, Voss EZ, Boldog FL, Malyankar UM; Padigaru M, Ji W, Smithson G, Edinger SR, Millet I, Ellerman K;
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                                                                                                                                                                                                                     Antidiabetic; anorectic; virucide; antibacterial; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 39; Page 233-234; 461pp; English.
                                                                                                                                                                NOVX related protein SEQ ID No 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-70N-2001, 200108-295739

12-70N-2001, 200108-297567P

14-70N-2001, 200108-297567P

14-70N-2001, 200108-297567P

15-70N-2001, 200108-299528F

15-70N-2001, 200108-299528F

15-70N-2001, 200108-299528F

15-70N-2001, 200108-399528F

21-70N-2001, 200108-301959F

28-70N-2001, 200108-301530P

03-70N-2001, 200108-301530P

12-8FP-2001, 200108-301530F

25-8FP-2001, 200108-301530F

26-70N-2001, 200108-301530F

27-70N-2001, 200108-301530F

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27-70N-2001, 200108-301530F

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2001US-296404P.
2001US-296418P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-2001; 2
06-JUN-2001; 2
06-JUN-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-2002;
                                                                                                          28-MAR-2003
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                                                     ABJ19379;
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RESULT 15 ABJ19379

Ge-1370 residue amino acid sequences, given in the specification, a mature form of them, or a sequence that is at least 95 # identical to, or chaving one or more conservative amino acid substitutions in one of the 35 amino acid sequences. The polypeptides, mucleic acid molecules and of an interesting a syndrome associated with a human disease, preferably a now-associated disorder. The mucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or disease, preferably a now-associated disorder. The mucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or disease, preferably a now-associated disorders, diabetes, obseity, infectious diseases. (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer associated cachexia, neurodegenerative disorders, Altheimer's disease, parkinson's disease, immune disorders, hematopoietic disorders, cancer and various dyslipidaemias, or metabolic disturbances associated with obseity, metabolic x syndrome, and wasting disorders. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. meurogenessis, call and angiogenesis, in gene therapy, in generation of antibodies that bind angiogenesis, in gene therapy, in generation of antibodies that bind angiogenesis, in gene therapy, in generation of antibodies that bind angiogenesis, in generation, and antibodies that bind angiogenesis, in generation of antibodies that bind angiogenesis, in generation, and each the acids are further used as hybridisation and pagnostic acids are further used as hybridisation and pharmacogenomics. This sequence represents a NOVX related protein of the

1162 AA; Sequence

Indels 142; Gaps Length 1162; Query Match 45.1%; Score 2364; DB 24; Best Local Similarity 50.3%; Pred. No. 8.2e-186; Macches 460; Conservative 116; Mismatches 197;

204 85 ASSSTRGAAGLDGKGRDMDEAGNHRSQQINTGTENQTLHVLTQYDLVSAYEVDHRGDYVS ASDSSSGASGLN------DOYNEVDSAGSYIS 47 à 셤 à

136 QK-PEVQQCFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLPQ-----LLA HEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSV QTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNSQ----KCPRDSVDFRAAQC 145 205

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261 AEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDG-----TPCSEDS 187 QEHNYSSPAG-HHPHVLYKRTAEEKIQRYRGYPG----SGRNYPGYSPSHIPHASQS R-----NVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRS 316

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441 407 501 467 561 527 621

APISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAG 348 LEQEPGGLLINHHADQSLNSFCQWQSALIGKNGKRHDHAILLTGFDICSWKNEPCDTLGF 442

------CAMKNEPCDTLGF

409

APISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNPCRKAEGNIMSPTLTG 502 RNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKWQFGE 468 NNGVFSWSSCSRQYLKKFLSTPQAGCLVDEPKQAGQYKYPDKLPGQIYDADTQCKAQFGA KAKLCMLDFKKDI CKALWCHRIGRKCETKFMPAABGTI CGHDMWCRGGOCVKYGDEGPKP 562 408

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622 THGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCBGSTRTLKLCNSQKCPRDS 588 IHGQWSAWSKWSECSRTCGGGVKFQERHCNNPKPQYGGLFCPGSSRIYQLCNINPCNENS

801 SPINKNDVCIDGVCELVGCDHELGSKAVSDACGVCKGDNSTCKFYKGLYLNQHKANEXYPV 767 VTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRRSYNE 861 VDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPC SEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHM PENLIATGPTNETLIVELLPQGRNPGVAWEYSMPRL--GTEKOPPA--QPSYT-----W 912 AIVRSECSVSCGGGR 926 ----STCSKACAGGQ 892 862 742 708 802 ద g 8 셤 8 à ò

completed: October 28, 2003, 23:40:52 Job time : 86 secs Search

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October 28, 2003, 23:26:49; Search time 46 Seconds (without alignments) 1990.274 Million cell updates/sec
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1 MKPRARGHRGLAALMMLLAQ......LEAACQPSATAYIALAFLES 952
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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IIRWNQIPDSHNKSVPHESNSNFAPMULXLDSEEEVROGMSRTDPDCTVRAHVKGVHO 224 NSPSHGGKFCEGSTRTLKLCNSGK. 224 NSPSHGGKFCEGSTRTLKLCNSGK. 31 HS	DD 292 WYEYHO-RELEDYULTLE-TVASITAHQSLRASINVOVALIVLKENASPKTIQHAQQ1 330	0 0 0 0 0 0 0 0 0 0	Qy 834 LNGHWTVDMP-GRYKESGTTFDYRRSYNEPENLIATGPTNETLIVELLFOGRN-PGVAWE 891	RESULT 3 T18517 Procollagen N-endopeptidase (EC 3.4.24.14) I - bowine N/Alternate names: procollagen N-proteinase C:Species: Bos primigaenius taurus (cattle) C:Species: Bos primigaenius taurus (cattle) C:Species: Bos primigaenius taurus (cattle) C:Species: Bos primigaense_revision 15-Oct-1999 #text_change 15-Oct-1999 C:Species: D. Nusgens, B.V.; Lapiere. C.M. submitted to the EMBL Data Library, February 1996 A:Description: Cloning of the CDNA of the bowine procollagen I N-proteinase. A:Reference number: 218941 A;Accession: T18517 A;Status: preliminary; translated from GB/EMBL/DDBJ
Db 361 TVCDPSRSCSVIEDDGLQAAFTTAHELGHVPNMPHD-DAKHCASLNGYTGDSHLMASMLS 419 Qy SOL GRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKWKYKYPEKLPGELYDANTOCKNOFG 560 420 SLDHSQPWSPCSRQYLHKFLSTAQAICLADQPKWKYKYPEKLPGELYDANTOCKNOFG 560 420 SLDHSQPWSPCSRQYLHKFLSTAQAICLADQPKBYKKYKPEKLPGELYDANTQCQFTFG 477 Qy S61 EKANLCHLDFKXDICKALWCHRIGRKCETKFWPAAGTICGHDWWCRGGQCVKYG 615	Cy 728 FFSISNKVBOTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVGGVCNGNNSACTIHRG 787	RESULT 2 191371 Hypotherical protein P25H8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: L5-Cdt-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T21371; T24896 R;Gajadety, S. R;Gajadety, S. R;Gajadety, S. R;Gajadety, S. R;Accession: T21377 A;Accession: T21377	A Seference to the EMBL Data Library, February 1996 A; Reference number: 129949 A; Accession: T24896 A; Accession: T24896 A; Accession: T24896 A; Accession: T24896 A; A; Accession: T24896 A; A; A; A; A; A; A; A; A; A; A; A; A; A	A;Gene: CESP:F25H8.3 A;Map position: 4 A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1; 81 Query Match Query Match Best Local Similarity 27.9%; Pred. No. 3.4e-61; Matches 264; Conservative 134; Mismatches 333; Indels 215; Gape 31; Qy 122 LHVLTQYDLVSAYEVDHRGDYVSHEIMHQRRRRAVANSEVESLHLELKGPRHDFHND 179 :

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GMCSKYRSCTINEDIGLAFTIAHESGHNFGMIHDGEGNMCKKSEG-----NIMSPTL 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67S QKCPRDS-VDFRAAQCAEHNSR-----RFRGRHYKWKP-YTQVEDQDLCKLYCIAEGFDF 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840 ---VDWPG--RYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYS-
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                                                                                                                                                                                                                                                                                                                                                  Length 837;
                                                                                                                                                                                                                                                                                 A;Gene: KIAA0688
C;Superfamily: thrombospondin type 1 repeat homology
F;519-575/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                            Query March 16.4%; Score 856.5; DB 2; Best Local Similarity 35.0%; Pred. No. 7.7e-54; Marches 219; Conservative 67; Mismarches 240;
                                                                                                                                                                                                                                                                                                                                                                                                      371 VETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKD---
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 KSEGNIMSPTLAGRNGVPSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGEL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KDGT----RHDHAILLTGLDICS 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        599 YDFQLCNSQDCFDALADFREEQCRQWDLYFEHGDAQ-----HHWLPHEHRDAKERCHLYC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRN-ALRRYYLNGHW 838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Wolecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1.1205 < COL.>
A, Festidues: 1.1205 < COL.>
A, SCROSS-references: EMIN. S98389, NID: 8990769; PID: e228215; PIDN: CAA65253.1
C; Genetics: A, Gene PC I-NP
C; Function: A, Gene PC I-NP
C; Punction: A, Gene PC I-NP
C; Reywords: hydrolase; metalloproteinase
C; Reywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                               DAĞGRLVSHVVSAATAPAGVRTRRAAPAĞIPGLSGGSEEDPGGRLFYNVTVFG--RDLHL
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                                                                                                                                                                                                      137 DHRGDYVSHEIMHHQR----RRRAVAVSEVESL-------HLRLKGPRHDFHM
                                                                                                                                                                                                                                                                 DLRTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTR
                                                                                                                                                                                                                                                                                                                         239 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-HYKW-KPYTQVEADLCKLYCIAEGFD
                                                                                                                                                                                                                                                                                                                                                    173 LIRMEBERFFIEPLEKGLAAKBAE-----QGRVHVVYHRPTTSRPPPL-----
                                                                                                                                                                                                                                                                                                                                                                                297 FFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                           357 KRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDGLMG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              667 RILKLCNSOKCPRDSVDFRAAQCA----EHNSRRFRGRHYKWKPYTQVEDQDLCKLYC
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                                                                                                                                               cch 18.15; Score 948; DB 2; Length 1205; all Similarity 29.7; Pred No. 3e-603; Indels 152; 269; Conservative 131; Mismatches 303; Indels 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 GSTRTLKLCNSQKCP-RDSVDFRAAQCAEHN----SRRFRGRHYKWKP-YTQVEDQDLCK 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833 YLNGHWTVDWPGR-YKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGR--NPGVA 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolccule type: DNA
A;Residues: 1.1444 <MIL>
A;Cross-references: EMBL:550004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone C02B4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                       A, Experimental source: adult melanoma (MeWo cell line); clone DKFZp762C1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 LICQAKGIGYFFVLQPKVVDGTPCSPDSTSVCVGQCVKAGCDRIIDSKKKFDKCGVCGG
                                                  20-Apr-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 550;
                      Cispecies: Howo sapiens (man)
Cispecies: Howo sapiens (man)
Cibace: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change:
Cibacession: T41186
Cispecies: An anureaschs, S.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, March 2000
A; Reference number: Z24379
A; Reterence number: Z24379
A; Reterus: preliminary
A; Residues: 1-550 < AAAA>
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C;Species: Caenorhabditis elegans
hypothetical protein DKFZp762C1110.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 731.5; DB 2; 36.0%; Pred. No. 4.9e-45; ive 61; Mismatches 197;
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submitred to the EMBL Data Library, July 1995
A.Refarence number: 219917
A,Accession: T24653
                                                                                                                                                                                                                                                                                    A,Cross-references: EMBL:AL162080
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 36.09
Matches 164; Conservative
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A;Note: DKFZp762C1110.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLCKLYCIAEGFDFFFSLSNKVKDG-TPCSEDSRNVCIDGICELS-------V 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 HHLNEEELKQVFGVSNKHDVPEYSLIEATRH------PLKNGNLKMKFTAWNDTYHLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 -AISDCGALMGSIVMEDHFLVLQTLPK------RVHHLQKERHLVYKRSAGLLTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 VSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 1444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: preliminary; translated from GB/EMBL/DUBU
A;MOJecule (Type: DNA PROPE)
A;Robicules: 1.1553, GKF' .GE2>
A;Rotoss-references: BMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A;Rotosis-references: strain Bristol N2; clone C37C3
C;Genetics:
C;Genetics:
A;Gene: CESP:C37C3.6b; CESP:C37C3.6a
A;Gene: CESP:C37C3.6b; CESP:C37C3.6a
A;Gene: CESP:C37C3.6b; CESP:C37C3.6a
A;HMap position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 458/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 GQCVKYGDEGPKPTHGH------WSDWSSWSPCSRTCGGGVSHRSRLCTNPK--- 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVD 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          722 AEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
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9.5%; Score 499.5; DB 2; Length 5
Best Local Similarity 33.9%; Pred. No. 6.1e-28;
Matches 111; Conservative 51; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

9.7%; Score 508.5; DB 2;
Best Local Similarity 33.6%; Pred. No. 3.9e-28;
Best Local Similarity 58; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 EEEVDYMYKFDNW----TPCSVSCGKG 360
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Rianonymous, The C. elegans Sequencing Consortium.
Science 262, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A5000; MUID:99069613; PMID:9851916
A;Note: see websites genome wmstl.edd/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: publiabled exrata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Scatus: preliminary
A;Scatus: preliminary
A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: appeared in Science 283, 2103, 1999; and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ and A;Scatus: ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Projects/ ac.uk/Proje
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A;Residues: 1-2167 <GEI>
A;Cross-references: BMBL;U64857; PIDN.AAC25868.1; GSPDB;GN00023; CESP:C37C3.6b
A;Experimental source: strain Bristol N2; clone C37C3
A;Accession: 734594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721
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C;8pecies: Caenorhabditis elegans
C;Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 01-Dec-2000
C;Accession: T34395; T34394
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C/Species: Caenorhabditis elegans
C/Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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                                                        QGRNPGVAWEYSMPRLGTEKQPPAQPSYT --- - WAIVRSECSVSCGGGR 926
                                                                                                           R---PCLIDQCSSKHLQEERPCDNEGCWTWWDEW----SSCSQSCGGGR 807
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submitted to the EMBL Data Library, July 1996
bescription: The sequence of C. elegans cosmid C37C3.
A;Reference number: Z21518
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A;Molecule type: DNA
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Db 142 HISSRP-CDLHCTTVDGQRQLAWPARDGTSCKLTDLRGVCVSGKCEPIGCDGWLFSTH 198 OY 768 VEDVCGVCNGNNSACTIHRGLYTRGHHTNQYYMWYIDSGARSIRIYEMNVSTSYISVTRN 827	SELT 10 Species and procesh T1902.1 - Caenorhabditis elegans Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acagas Species acanonhabditis acapas Species acanonhabditis acapas Species acanonhabditis acapas Species acanonhabditis acapas Species acanonhabditis acapas Species acanonhabditis acapas Species acanonhabditis acapas Species acanonhabditis acapas Species acapas Speci	Db 477 IRQCNNFSSNNGGAPCGÓDEARGAVCHRDVĆNGDŚIENYÁTRVCSRLÄDBNAIP 530 Qy 707 YTQVEDQDLCKLYCIAEGEPDFFSLSNKVKDGTPCSBDSRNVCIDGICERVGG- 759

DD	Db 458 EDTGLGLAFTIAHESGHNFGMIHDGEGNMCKTGSEGNIMSPTLAGRNGVFSMS 509 458 EDTGLGLAFTIAHESGHNFGMIHDGEGNMCKTGSEGNIMSPTLAGRNGVFSMS 509 314 QDHSKNSIGVASTWAHELGHNLGMSHDEDIPGCYCPEPREGGGIMTESI -GSKFPRIFS 372 Qy 510 PCRQVLHKFLSTAGAICLADDPKPWEDYKYPEKLPGELYDANTQCKWQFGEK 562
change 26-Aug-1999 amamoto, S. a novel cell surface antigen st	Qy 757 VGCDVLGSDAVEDOCCVGNANSCITIRG 787 Qy 757 VGCDVLGSDAVEDOCCVGNANSCITIRG 787
C;Superfamily: mouse meltrin alpha; disintegrin homology C;Superfamily: mouse meltrin alpha; disintegrin homology C;Keywords: glycoprotein; surface antigen; transmembrane protein F;1-14/Domain: signal sequence #status predicted <sig> F;402-484/Domain: signal sequence #status predicted <sig> F;569-683/Domain: transmembrane #status predicted <twm> F;530/Active site: Glu #status predicted Cquery Match 5.8%; Score 305; DB 2; Length 826; Best Local Similarity 21.6%; Pred. No. 5.9e-14; Matches 163; Conservative 79; Mismatches 238; Indels 274; Gaps 37;</twm></sig></sig>	A;Accession: 722836 A;Accession: 722836 A;Accession: 722836 A;Accession: preliminary; translated from GB/EMBL/DDBJ A;Accession: 1508 cMIL> A;Residues: 1-508 cMIL> A;Residues: 1-508 cMIL> A;Residues: 1-508 cMIL> A;Cross-references: BRBL:274037; PIDN:CAA98493.1; GSPDB:GN00023; CESP:F57B7.4 A;Reperimental source: clone F57B7 C;Genetics: A;Reperimental source: clone F57B7 A;Reperimental source: clone F
152 RRRRAVAVSEVESLHIRLKOPRHDFHMOLRTSSSLVAPGFIVQTLGKTGTKSVQTLP	Query Match 5.5%; Score 289; DB 2; Length 508; Best Local Similarity 23.8%; Pred. No. 4.6e-13; Matches 129; Conservative 70; Mismatches 188; Indels 158; Gaps
OY 209 PEDFORMANDENENDANDENENDANDENENDANDENDENDENDDEND	OY 198 KTOTKSVOTLEPEDFCFYQSIRSHRNSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRA 257
	96AIHNIKEYLHALFEQTKIIYDGISFGNETLHWVFAGTWIATOERD 318 VCIDGICELSVVSTSAHMPQPFEGLFILPDEXKSCLEHKRSLLRSHNB :
QY 376 VVDKKAMQNHG-HENITTYULILINMVSALFKD	QY 368 ELNVETLYVVDKROMQNHGHENITTYVLTILNNVSALFKDGLMGKDGTR 416

	: : :	Db 381 YNXYLKYNPKCILDPPLR-KDIASPAVGANEIWEGGECDCGSPADCRNPCC 432 Qy 576 KALWCHRIGKCETKEMPAAEGTICGHDWMCRGGQCWKYGDEGEFPTHGHWSD 628 433 DAATC
Oy 688 DC 689 Db 497 CC 498 RESULT 14 RESULT 14 Species: Echis carinatus (saw-scaled viper) C;Detei: Schis carinatus (saw-scaled viper) C;Detei: OS-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 21-C;Accession: A55796 Rivishida. T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya Riochemistry 34, 1771-1778, 1995 Rivishida. T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya Riochemistry 34, 1771-1778, 1995 Rivishida. T.; Rohno, N.; Atoda, H.; Morita, T.; Takeya Riochemistry 34, 1771-1778, 1995 A;Accession: A55796; MUID:95151760; PMID:7849037 A;Accession: A55796 A;Accession: A5796 A;Accession: A5796 A;Accession: A5796 A;Accession: A5796 A;Accession: A5796 A;Acces	hange 21-Jul-2000 .; Takeya, H.; Kido, I.; Paine .cothrombin activator (ecarin) 1; PID:g717091	REGULT 15 \$48167 metalloproteinase (EC 3.4.24) H-I precursor - carpet viper N; Contains: disincegrin C; Species: Edils pyramidum leakey; C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Ju1-2000 C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Ju1-2000 C; Accession: 848160 R; Pains, M.J.I.; Moura-La-Silva, A.M.; Theakston, R.D.G.; Crampton, J.M. Eur. J. Biochem. 224, 4831-488, 1994 A; Title: Cloning of metalloprotease genes in the carpet viper (Echis pyramidum leakey; A; Actors—references: 488160 A; Molecule trype: mRWA A; Reference number: 848160 A; Molecule trype: mRWA A; Cross-references: GB:X78970; NID:G763092; PIDN:CAA55565.1; PID:G763093 C; Superfamily: mouse metalloproteinses vanom C; Superfamily: mouse metalloproteinses vanom C; Superfamily: mouse metalloproteinses vanom F; 11870-main: signal sequence #status predicted <rro> F; 193-617/Porduct: metalloproteinses wanom F; 1403-485/Domain: disintegrin homology <is> F; 103-485/Domain: disintegrin homology <is 103-485="" 104-48-48-48-48-48-48-48-48-48-48-48-48-48<="" <is="" disintegrin="" domain:="" f;="" homology="" td=""></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></is></rro>
Query Match		Similarity 18.9%; Pred. No. 4.1e-11; KSYOLPE-DPFYOGELESHENEPSHGRECEGSTRITE KSYOLPE-DPFYOGELESHENEPSHGRECEGSTRITE KSYOLPE-DPFYOGELESHENEPSHGRECEGSTRITE KSYOLPE-DPFYOGENERSHENEPSHGRECEGSTRITE KSYOLPE-DPFYOGENERSHENEPSHGRECEGSTRITE KSYOLPE-DPFYOGENERSHOPPSHGRENESHENE AEHNSERERGHYKMKPYTOVEADLCKLYCIAEGNEFFSH GYPHIRGETYLIEPLIPESEAHAY;

à i	580 CHRIGRKCETKEMPAAEGTICGHDMWCRGGQCVKYGDEGPKPTHGHWSDWSSWSPC 635	10
g	407 CGNYFVEVGEECDCGSRTYCR	0
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ф	431GNATICKLTPGSQCADGECC 450	
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δ	749 CIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHTNQ 797	4
QQ	501 CYNGNCPILKNQCIHLWKPAPPAGVNVAPDVCFEDNQNGTDVYNGGIKNGTYIKCARQD- 559	0.
ò	798 YYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRR 857	,
Op	560IKCGRL 565	:0
ò	858 SYNEPENLIATGPINETLIVELLEQGRNPGVAMEYSMPRLGTE 900	
g	566 SCEEPSTGNTINCQAPFSSRNPDYGWVDIGTK 597	

Search completed: October 28, 2003, 23:46:01 Job time : 50 secs

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OM protein - protein search, using sw model

October 28, 2003, 21:53:59; Search time 48 Seconds (without alignments) 932.696 Willion cell updates/sec Run on:

5236 1 MKPRARGWRGLAALWMLLAQ.......LBAACQPSATAYIALAFLES 952 US-09-981-151A-8 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CTAMMADIES

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SUMMARIES		ΩI	AT18 HUMAN	AT10 HUMAN	ATS6 HUMAN	AT12_HUMAN	ATS7 HUMAN	AT20 MOUSE	ATS9 HUMAN	AT20 HUMAN					AT19 MOUSE	AT17 HUMAN	ATS1_HUMAN	ATS2 BOVIN	ATS2 HUMAN	AT15 HUMAN	AT14 HUMAN	ATSS_MOUSE	ATS5_HUMAN	ATS4 RAT	ATS4_HUMAN	ATS8_MOUSE	ATS8 HUMAN	AT15_MOUSE	ATSS_BOVIN	ATS4_BOVIN	AD19_MOUSE	AT10_MOUSE	AD19_HUMAN	AD08_HUMAN	AD08_MOUSE
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## ALIGNMENTS

RESULT

NCBI_TaxID=9606;

MEDLINE=21855482; PubMed=11867212; 251 S., Daya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otio C.,

"Cloning, expression analysis, and structural characterization of

seven novel human ADANTES, a family of metalloproteinases with distinged and thrombospondin-1 domains."; dene 283:49-62(2002).
-!- COPRACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- COPRACTOR: Expressed in fetal lung, liver, and kidney metrix (By similarity).
-!- TISSUE SPECIFICITY: Expressed in fetal lung, liver, and kidney and in adult brain, prostate, submaxillary gland, and endothelium.
-!- FIM: The precursor is cleaved by a furin endopeptidase (By similarity).
-!- SIMILARITY: Enlongs to peptidase family N12B.
-!- SIMILARITY: Contains 1 disintegrin-like domain.

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MIN, 607312; ...
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INTERPRO; IFROUGES, PED WIZE PROPED.
INTERPRO; IFROUGES, PED WIZE PROPED; 1.
PEAM; PRO1421, REPRO14S11, 1.
PEAM; PRO0509; 15P1; 4.
PROSITE; PS00209; TSP1; 4.
PROSITE; PS00215; ADAM WERRO; 1.
PROSITE; PS00454; CYSTEINE SMITCH; FALSE NEG.
PROSITE; PS00454; CYSTEINE SMITCH; PALSE NEG.
PROSITE; PS00415; DISINYEGRIN 1; PALSE NEG.
PROSITE; PS014; DISINYEGRIN 1; PALSE NEG.

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VDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPC
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InterPro; IPRO01762; Per Mills propep.
InterPro; IPRO01639; Reprolysin.
InterPro; IPRO00684; TSP1.
InterPro; IPRO00625; Zn Wilpeptdse.
Pfam; PPO1562; Pep Mills propep; 1.
Pfam; PP01421; Reprolysin; 1.
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TSP TYPE-1 4.
TSP TYPE-1 4.
TSP TYPE-1 4.
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ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
JINCE (GIGNAC. .) (POTBWILAL).
N-LINKED (GIGNAC. .) (POTBWILAL).
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                     Glycoprotein; Zymogen;
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ADAMTS-18.
METALLOPROTEASE.
DISINTEGRIN-LIKE.
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CYS-RICH.
SPACER.
  PROSITE; PS50092; TSP1; 3.
PROSITE; PS00147; ZINC; PROTEASE; FALSE NEG.
Hydrolase; Metalloprocease; Zinc; Signal; C
Repeat; Extracellular matrix.
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                                                                                                                                                                                                                                                                                                                SPINGNDYCIDGVCELVGCDHELGSKAVSDACGVCKGDNSTCKFYKGLYLNQHKANEXYPV 766
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DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By similarity).
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Apm-TSIO: a novel member of the ADAM-TS family containing multiple thrombospondin type I repeats.";

Submitted (JUN-1999) to the EMEL/GenBank/DDBJ databases.

-: COFACTOR: BINDS: INCY INN (BX SIMILARITY).

-: SUBCELLULAR LOCATION: Secreted, Associated with the extracellular.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
48-FEB-2003 (Rel. 41, Last annotation update)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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EMBL; AF140674; AAD56357.1; -.
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(C. .) (POTENTIAL).
(C. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.4%; Score 1223; DB 1; Length 1077;
PÉAM; PP00090; tSP_1; 5.
SMART; SM00209; TSP_1; 5.
PROSITE; PS50215; ADAM MERRO; 1.
PROSITE; PS50215; DISINTEGRIN 1; FALSE NEG.
PROSITE; PS500427; DISINTEGRIN 2; FALSE_NEG.
PROSITE; PS50042; TSP1; 5.
PROSITE; PS50042; TSP1; 5.
PROSITE; PS0042; TNC PROTEASE; 1.
Hydrotase; Metalloptotease; Zinc; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 N-LINKED (GLCNAC. . .) (POT)
118072 MW; 3914DE18DCBBF587 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                                                                                                                                                                                                        METALLOPROTEASE.
DISINTEGRIN-LIKE
                                                                                                                                                                                                                                                                                                                                     TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
                                                                                                                                                                                                                 SIMILARITY.
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769 76
866 86
1077 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this stetement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                  463 QCKYG---EVCSELMCLSKSNRCITNSIPAAEGTLCQTHTIDKGWCYKRVCVPFGSR-PE 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 LCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTIC-GHDM---WCRGGQCVKYGDEGPK 620
                                                                                                                       621 PTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGSTRTLKLCNSQKCPRD 680
                                                                                                                                                             519 GVDGAMGPWTPWGDCSRICGGGVSSSSRHCDSPRPTIGGKYCLGBRRRHRSCNTDDCPPG 578
                                                                                                                                                                                                                                                 SVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTP 740
                                                                                                                                                                                                                                                                                                741 CSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYH 800
                                                                                                                                                                                                                                                                                                                                                                                                                       638 CRPDITVDICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYED. 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 MVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRRSYN 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 VVWIPKGSVHIFIQDLNLSLSHLALKGDQESLLLEGLPGTPQPHRLPLAGTTFQLRQGPD 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861 EPENLIATGPTNETLIVELLFQGRNPGVAWEYSMPRLGTEKOPPAOPSYTWAIVR-SECS 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-DOCT-2001 (Rel. 40, Last amoutation update)
ADAMTG-6 precursor (RC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 6) (ADAM-TS 6) (ADAM-TS6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enkaryota, Metazoas, Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-- SIMILARITY Belongs to peptidase family M12B.

--- SIMILARITY: Contains 1 disintegrin-like domain.

--- SIMILARITY: Contains 2 7SP type-1 domains.
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422
330 KSILSHQSDGNTIPENGIAHHDNAVLITRYDICTYKNKPCGTLGLASVAGMCEPERSCSI 389
                                                           NEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAGRNGVFSWSPCSRQYL 516
                                                                                                                                                                                                                                                              ------KVMKQ----QNYGSSHYĆEYQ--SFFLVCLQSRXHHQLF 455
                                                                                                                                                                                                                                                                                                                             627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRN 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRRSYNEPENLIA 867
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAMTS-12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-TS12).
                                                                                                                                                                                          517 HKFLSTAQAICLADQPKPVKEXKYPEKLPGELYDANTQCKWQFGEKAKLCML----DFK
                                                                                                                                                                                                                                                                                                                         572 KDICKALWCHRIGRKCETKFMPAAEGTICG----HDWWCRGGQCVKYGDEGPKPTHGHWS
                                                                                                                                                                                                                                                                                                                                                                 DOWAIN: THE SPACER DOWAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CADPDNMPPRGKYYNWKPYTGGGVKP-CALNCLAEGYNFYTERAPAVIDGTQCNADSLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal lung;
MEDLINE=21864577; PubMed=112790865,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         694 SVHIEVREVAMSKNYIALKSEGDDYYINGAWTIDWPRKFDVAGTAFHYKRPTDEPESLEA
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PIW: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       390 NEDIGLGSAFTIAHEIVHNFGMNHDGIGNSC------GR-----
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TISSUE SPECIFICITY: Exp.
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P58397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 HRSQQTNTGTENQTLHVLTQYDLVSAXEVDHRGDYVSHEIMH--HQRRRRAV----AVSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 VSKLFFKLSAYGKHFHINLTINTDFVSKHFTVEYWGKDG-------PQWKHDFLDNCHY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 VSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKAMQNHGHE 388
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270 DIEHYILSVMNIVAKLYRDSSLGNVVNIIVARLIVLTEDQPNLEINHHADKSLDSFCKMQ 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 VESLHIRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSVQTLPPE-----DFCFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 TGYLQDQRSTTKVALSNCVGLHGVI-----ATEDEEYFIEPLKNTTEDSKHFSYENGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 PHVIYKKSALQQRHLYDHSHC-----GVSDFTRSGKPWMLNDTSTVSY----SLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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PROSITE: PSO0142; ZIMC_PROTEASB; 1.
PROSITE: PSO0042; TSP1, 1.
PROSITE: PSO0427; ISB1, 1.
PROSITE; PSO0417; INSINTEGRIN 1; PALSE NEC.
PROSITE; PSSO414; INSINTEGRIN 2; PALSE NEC.
HYGROLASE; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
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al Similarity 31.7%; Pred. No. 3.8e-80;
286; Conservative 131; Mismatches 291; Indels 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC) (BY SIMILARITY)
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ADAMTS-6,
METALLOPROTEASE,
DISINTEGRIN-LIKE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP TYPE-1 1.
CYS-RICH.
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                                                                                   MIM, 605008; -. .
Interpro, IRR001762, Disintegrin.
InterPro, IRR0018070; Pep M12B_propep.
InterPro, IRR001804; Reprolysin.
InterPro, IRR001804; TSP1.
InterPro, IRR006804; TSP1.
InterPro, IRR006052, RayPropedse.
Pfam; PF01562; Pep M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
SMART, SM00209; TSP1, 1.
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                   MEROPS; M12.230; -. Genew, HGNC:222; ADAMTS6.
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TO A FRACEBY CONTAINING THE N-TERNINAL REGION INCLUDING THE METALLOROFICHMASE, DISINTEGRIN-LIKE, YGF-RICH AND TS-1 DOMAINS AND THE C-TERNINAL FRACER 2 AND THE FOUR TS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0427; DISINTEGRAN, 1; FALSE NEG.
PROSTE; PSSO044; DISINTEGRAN, 1; FALSE NEG.
PROSITE; PSSO092; TSP1; 6.
PROSITE; PSO0142; ZINC_PROFISES; 1.
Hydrolase; Mealloprofease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
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                                                                                                                                   -!- SIMILARITY: Belongs to peptidase family M12B.
-!- SIMILARITY: Contains 1 distintegrin-like domain.
-!- SIMILARITY: Contains 1 PLAC domain.
-!- SIMILARITY: Contains 8 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM' 606184;

InterPro; 1PR001762; Disintegrin.
InterPro; 1PR001870; Reprolysin.
InterPro; 1PR001890; Reprolysin.
InterPro; 1PR001890; Reprolysin.
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BY SIMILARITY.
ADAMTS-12.
METALLOPROTEASE.
DISINTEGRIN-LIKE.
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SPACER 2.
TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 8.
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TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
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                                                                                                                                                       49 LPEYHVVGPVRVDASGHPLSYGLHYPITSSRRKRDLDG9E-DWVYYRISHEEKDLFFNLT 107
                                                                                                                                                                                                    182 TSSSLVAPGFIVQTL--GKTGTKSVQTLPPEDFCFYQGS-LRSHRNSPSHGGKFCEGSTR 238
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                                                                                                                                                                                                                                                                       239 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRH----YKWKPYTQVEADLCKLYCIAEG 294
                                                                                                                                                                                                                                                                                                             16 FFOLPHG-----DFFIEPVKKHPLVE-GGYHPHIVYRRQKVPETKEPTCGL---- 210
                                                                                                                                                                                                                                                                                                                                                295 FDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCL 354
                                                                                                                                                                                                                                                                                                                                                                                                                   355 RH---KRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDGLMG 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
1503 1503 N-LINKED (GLCNAC. . .) (POTENTIAL)
1593 Aa; 177545 MW; 07P9P48B63BDB3A3 CRC64;
                                                   Query March 23.0%; Score 1205.5; DB 1; Length 1593; Best Local Similarity 33.3%; Pred. No. 1e-79; Matches 288; Conservative 131; Mismatches 311; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          997 AA.
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129 DLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVA 188
                                                                                                                                                                                                         DIVHPVRVDAGGSFLSYELWPRALKKRDVSVRRDAPAFYELOYRGRELRFNLTANOHLLA 103
                                                                                                                                                                                                                                                                                                                                                                294 GFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSC 353
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                                                                                                                                                                                                                                        PGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGG----KFCEGSTRTLKLCN
                                                                                                                                                                                                                                                                      PGFVSETRRRGGLGRAHIRAHTPACHLLGEV---QDPELEGGLAAISACDGLKGVFQLSN
                                                                                                                                                                                                                                                                                                       SQKC--PRDSVDFRAAQCAEH-----NSRRFRGRHYKWKPYT---QVEADLCKLYCIAE
                                                                                                                                                                                                                                                                                                                          EDYFIEPLDSAPARPGHAQPHVVYKRQAPERLAQRGDSSAPSTCGVQVYPEL-----
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                                    N.LINKED (GLCNAC. . .) (POTENTIAL)
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N.LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                             Best Local Similarity 30.5%; rreu. No. >.oe ./,
Matches 294; Conservative 125; Mismatches 305; Indels 240;
                                                                                                                22.7%; Score 1189; DB 1; Length 997;
                                                                                 109694 MW; 6587044ED02FC104 CRC64;
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                                                                                                                                                                                                                                                                                  matrix (By similarity).
TISSUE SPECIFCITY: EXPRESED IN HEART, BRAIN, FLACENTA, LUNG,
LIVER, SKELETAL MUSCLE, KIDNEY, PANCRERS.
DONAIN: THE SPACER DOWAIN AND THE TSP TYBE: I DOWAINS ARE IMPORTANT
POR A TIGHT INTERACTION WITH THE EXTRACEL/LULAR MATRIX.
PTM: THE PREVISOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                                                                                                     zinc metalloproteases.";

2 inc metalloproteases.";

3 isid. (Emm. 274:25555-25631(1999).

4 : CoFACTOR: Binds 1 zinc per subunit (By similarity).

-! SUBCELLULAR LOCATION: Secreted, Associated with the extracellular
                                      metalloproteinase
                                                                                                                                                                         WEDLINE-99395124; PubMed=10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
*ADAM-TSS, ADAM-TSS, and ADAM-TSS, novel members of a new family of
                                                                            Homo sapiens (Human).
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PSO0142, ZINC_PROFEASE, 1.
PROSITE, PSO0142, DAM NEPO., 1.
PROSITE, PSO0427, DAM NEPO., 1.
PROSITE, PSO0427, DISINTEGRIN_1; FALSE NEG.
PROSITE, PSO0427, DISINTEGRIN_1; FALSE_NEG.
PROSITE, PSO0921, TOSINTEGRIN_2; FALSE_NEG.
PROSITE, PSO0921, TSP1, 1.
PATOLASE; MERALLOPTOLESSE, Zinc, Signal; Glycoprotein; Zymogen; Sepeat, Extracellular matrix. POTENTIAL.

27 POTENTIAL.
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAMTS-7 precursor (EC 3.4.24.-) (A disintegrin and me with thrombospondin motifs 7) (ADAM-TS 7) (ADAM-TS).
                                                                                                                                                                                                                                                                                                                                                                                         -:- SIMILARITY: Belongs to peptidase family M128.
-:- SIMILARITY: Contains 1 disintegrin-like domain.
-:- SIMILARITY: Contains 1 PLAC domain.
-:- SIMILARITY: Contains 2 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISINTEGRIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
ADAMTS-7.
METALLOPROTEASE.
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TSP TYPE-1 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IRR002162; Disintegrin.
InterPro; IRR00280; Pep MI2B propep.
InterPro; IRR002804; TSP1.
InterPro; IRR006804; TSP1.
InterPro; IRR006082; Zn Mrpeptdse.
Pfam; PF01562; Pep MI2B propep; 1.
Pfam; PF01421; Reprolysin; 2.
Pfam; PF000090; TSP1, 2.
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                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=9606;
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873 RRHLVLMGPRLPTQLLFQESNPGVHYEYTIHREAGGHDEVPP--PVFSWHYGPWTKCTVT 930
                                                                                                                                                                                                                                                                                                                                           Liamazares M., Call S., Lopez-Otin C.;
Liamazares M., Call S., Lopez-Otin C.;
Indertification and characterization of ADAWTS-20 defines a novel
subfamily of metalloproteinsses-disintegrins with multiple
thromospondin-1 repeats and a unique GON-domain.",
Submitted (OCT-2002) to the EMBL/GenBank/DBU databases.
i. FUNCTION: May play a role in tissue-remodeling process occurring
in both normal and pathological conditions.
in both normal and pathological conditions.
i. CORACTOR: Binds 1 zinc ion per submit (By similarity).
i. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                          (ADAM-TS 20) (ADAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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PROSITE; PS50024; TSP1, 13.
PROSITE; PS00142; ZINC PROTEASE, 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix. POTENTIAL.
                                                                                                                                                   15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
metalloproteinase with thrombospondin motifs 20) (App
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SMART, SM0209; TSP1, 14.
PROSITE: PSC0215; ADA MERRO, 1.
PROSITE: PSC0427: DISINITECRIN 1; FALSE NEG.
PROSITE: PSC04214; DISINITECRIN 2; FALSE NEG.
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P59511;
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ò 9	183	SSSLVAE :::  DAAFLA	SSSLVAPGFIVQTLGKTGTKSVQT 	TGTKSVQT   :  :: PGPGGRSTES	TGTKSVQTLPPEDFCFYQGSLRSHRN   :	QGSLRSHRNS :  : : RGQVNARED-	SPSHGGKF    HTAVFSL	CEGS 2	36
දු පු	237	TRILKLO	TRTLKLCNSQKCPRDSVDFRA 	1 8	EHNSRRFRG :   DHN	RHYKWK	-AQCAEHNSRRFRGRHYKWKPYTQVEADLCKLYC 	CIAE 2	92
 & g	193	GPDFFFSLSNK  : :  NSFARSHK	VKDGTP	C	SEDSRNVCIDGICE 	vcibgi   Trobvb	LSVVSTSAHMP	OPPK 3	30
 ò 8	341	EDLFILPDE   :    EAVFRLEGE	YKSCLRHKR	SLLRSHRNEEL 	YPR	LVVVDK :    MVTADA	VETLVVVDKKMMQNHGHENITTY    :        :         PRYVEVMVTADAKMVHHG-QNLQHY	VLT VLT	396
 \$ Q	397	ILNMVSP :::: :  LMSIVAP	ILNWVSALFKDGLMG :::: : : :  LMSIVAAIYKDSSIGNLI	G   GNLINIVIVKLVVIH	KDG ::  SEQEGPVI	SFNAAT	SFNAATTLRNFCLWQQSQNVPDD	4 W	14
که م م	415	TRHE         AHPSHHE	TRHDHAILLTGLDICSWRNEPCDTL :	SWKNEPCDTL 	EPCDTLGFAPISGMCSKYRSCTI 	SKYRSC     DPSRSC	SCTINEDIGLGLAFTIJ   : : :    SCSISEENGLSAAFTIJ	CHE 4	71
 <u>ک</u> ۾	472	SGHNFGM      : LGHVFNV	IHDGEGNMCK-    :    PHD-DSFKCKE	AGIKHQYHVMA	SPTLAGRNGVFSWS:      	VFSWSP ::   PWTWSA	PCSRQYLHKFLSTAQAI   :::::    acsqkhitefldtghge	ე — ი შ 4	27
 % a	528	LADQPKP    :  LLDKPNG	VKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDI	SELYDANTOCI   :        SSVYDGNRQCI	KWQFGEKAKL:::  :::	CCMLDF:  -  - VCPY	CKALWC  :     CRRLWCTSA	IG S WH S	84
 oy Oy	585	RKCETKF :    : KGCRTQH	BTKFMPAAEGTICGHI  :   :   RTQHMPLADGTSCGPO	CGHDMMCRGQCVKXGDEGPKPTHGHMSDMSSWS  	CYGDEGPKP)   :   -RDMETRP	THGHWS     VDGEWG	DWSSWSPCSRTCGGG'   :          PWGPYSSCSRTCGGG	6 2 3 1 1 6 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	44
දු පු	645	HRSRLCTNI :       STARLCDRI	PKPSHGGKF  : : :: PEPRNGGRY	CEGSTRILKLCNSQKCPRDSVD	ASQKCPRDSV 	VDFRAA       PDFREK	NSRRFRGRH	7 7	2 0 2

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                                                                                                                                                                                                                   (POTENTIAL)
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Short).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
           SIMILARITY: Belongs to peptidase family M12B.
SIMILARITY: Contains 1 disintegrin-like domain.
SMILARITY: Contains 12 TSP type-1 domains.
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(GLCNAC...)
(GLCNAC...)
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(BY
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TSP TYPE-1 1.
TSP TYPE-1 2.
CYG-RACH.
SPACER.
TSP TYPE-1 4.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 10.
TSP TYPE-1 10.
TSP TYPE-1 11.
TSP TYPE-1 11.
TSP TYPE-1 11.
TSP TYPE-1 11.
TSP TYPE-1 11.
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N-LINKED (GLCNAC.
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BY SIMILARITY.
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ZINC (CATALYTIC)
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N-LINKED (
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                                                                                                                                                                                       MEROPS; M12.021; -.
Genew; HGNC:13202; ADAMTS9.
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SIMILARITY)
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METAL
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868
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                                                         814
                                                                                                                                                    869 GPTNETLIVELLFOGR--NPGVAWEYSMP---RLGTEKQPPAQPSYTWAIVRSECSVSCG 923
                                                                               690 RQAGCDHVLNSKAKRDKCGVCGDNSSCQTLAGVFNSAHY--GYNVVVKIPAGATNIEIL 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                             ATS9 HUMAN STANDARD; PRT; 1629 AA.
DSPAR, GONR29;
16-COT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
ADAMTS-9 precursor (EC 3 4 .24 .24 ...) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAM-TS 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.; Prediction of the coding sequences of unidantified human genes. XVI. The complete sequences of 150 new CDNA clones from brain which code for large proteins in vitro."; DNA Res. 7:65-73(2000).
--- CORACTOR: Binds 1 zinc ion per subunit (By similarity).
--- SUBCELIGAR LOCATTON: Secreted. Associated with the extracellular matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOId=G9P2N4-2; Sequence=VSP_005499, VSP_005500;
NOC=NO experimental confirmation available;
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES.
EXPRESSED SLIGHTLY HIGHLY EXPRESSED IN ALL FETAL LING:
PLACENTA ALSO DETECTED IN SULMA. CORD AND BRAIN. NOT DETECTED IN COLON, SMALL INTESTINE, IESTIS, LIVER, SKELETAL MISCLE. SPLEED OCCON,
            -----KWKP-YTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGIC
                         ERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIY
                                                                                                       EMNVS-----TSYISVRNALRRYYLNGHWTVDWPGR-YKFSGTTFDYRRSYNEPENLIAT
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
ENdaryocar, Menazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maki R.A.;
"ADAWTS 9, a novel member of the ADAM-TS/Metallospondin gene
familv.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 159-1629 FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Long;
IsoId=Q9P2N4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=20181126; PubMed=10718198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20396138; PubMed=10936055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 67:343-350(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 PVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIG---RKCETK 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 FMPAAEGTICGHDMWCRGGQCVKYGDEGPKPTHGHWSDMSSWSPCSRTCGGGVSHRSRLC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 TNPKPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHY----- 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            616 NRPEPKNGGKYCVGRRMKFKSCNTEPCLKQKRDFRDEQCA-----HFDGKHFNINGLLPN 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              761 NVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVS- 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          731 HVLNSKARRDKCGVCGGDNSSCKTVAGTFNTVHY--GYNTVÝRIPAGATNIDVRQHSFSG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TSYISVRNALRRYYLNGHWTVDWPGR-YKFSGTTFDYRRSYNEPENLIATGPTNET 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 RDMDEAGNHRSQQTWIGTENQTLH -----VLTQYDLVSAYEVDHRGDYVSHEIMHQ 151
                                                                                                                                                                                              152 RERRAV------AVSEVESLHIRLKGPRHDFHMDLRTSSSLVAPGFIVQTLG 197
                                                                                                                                                                                                                        71 RTRRSINSATOPWPAFASSSSSTSSQAHYRLSAFGQQFLFNLTANAGFIAPLFTVTLLG 130
                                                                                                                                                                                                                                                                                131 TPGVNQTKFYSEEEAELKHCFYKGYVNTNSEHTAVISLCSGMLGTFRSHDGDYFIEPLQS 190
                                                                                                                                                                                                                                                                                                            234 -----EGSTRTLKLCNSQKCPR--DSVDFRAAQCAEHNSR----RFRGRHYKWKPYTQV 281
                                                                                                                                                                                                                                                                                                                                     191 MDEQEDEEEQNKPHIIYRRSAPQREPSTGRHACDISEHKNRHSKDKKKTRARKWGERINL 250
                                                                                                                                                                                                                                                                                                                                                                   282 EADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKE 341
                                                                                                                                                                                                                                                                                                                                                                                             251 AGDVAALM-----SGLATEAFSAYGNKT 273
                                                                                                                                                                                                                                                                                                                                                                                                                         342 DLFILPDEYKSCLRHKRSLLRSHR--NEELNVETLVVVDKKOMQNHGHENITTYVLTILN 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 D. ...----NTREKRIHRRTKRFLSYPRFVEVLVVADNRAVSYHG-ENLQHYILTLMS 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 IVASIYKDPSIGNLINIVIVNLIVIHNEQDGPSISFNAQTTLKNFCQWQHSKNSPGGIHH 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 MIHDGEGNMCK----KSEGNIMSPTLAGRNGVPSWSPCSRQYLHKFLSTAQA1CLADQPK 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 MPHD-DNNKCKEEGVKSPQHVMAPTLNFYTNPMMSKCSRKYITEFLDTGYGECLLNEPE 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 HTPWADGIECEPGKHCKYGFCVPKEMDVP-VIDGSWGSWSPFGTCSRICGGGIKTAIREC 615
                                                                                                                                                                15 RDLAEMG---SPDAAAAVRKDRLHPRQVKLLETLGEYEIVSPIRVNALGEPFPTNV-HFK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 KTGTKSVQTLPPED----FCFYQGSLRSHRNSP-----SHGGKFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 - KWKP-YTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCD
                                                                                                              Gaps
                                                                                                              Conservative 148; Mismatches 334; Indels 253;
                                                                              20.3%; Score 1061.5; DB 1; Length 1629; Similarity 27.6%; Pred. No. 3.3e-69;
        1073 1629 Missing (In isoform short).

37 367 F- L (IN REF 1).

1629 AA; 182649 MW; CIC4CEFF58B8941F CRC64;
FTIG=VSP 005499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 MVSALFKDGLMGK--------
                                                                                                               Matches 280;
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               VARSPLIC
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Best Local
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Decrease in State institutes institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- TISSUB SPBCIRCITY: Very sparingly expressed, although is detected at low levels in testis, prostate, cowary, heart, placenta, lung and pancreas. Overexpressed in several brain, colon and breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liamazares M., Cal S., Lopez-Otin C.;
"Identification and characterization of ADAMTS-20 defines a novel
"Identification and characterization of ADAMTS-20 defines a novel
subfamily of metalloproceinasses-disintegrins with multiple
thrombospondin-1 repeats and a unique GON-domain.",
submitted (NOV-2002) to the RNBL/Gensamk/DDBJ databases.
-i. FWNCTION: May play a role in tissue-remodeling process occurring
-i. FWNCTION: May play a role in tissue-remodeling process occurring
-i. CORACTOR: Binds 1 zinc ion per subunit (By similarity)
-i. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
-i. ALPRANIUS PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
ADMMTS-20 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 20) (ADAM-TS 20) (ADAM-
905 ------AQPSY-----TWAIV-RSECSVSCG-GGRCLPV 930
                                                               906 RESDQLTVSDQRCDRLPQPGHITEPCGTDCDLRWHVASRSECSAQCGLGYRTLDI 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Somerville R.P., Longpre J.-M., Jungers R.A., Engle J.M., Ross M., Bvanko S., Might T.N., Leduc R., Apte S.S.; "Characterization of ADAMTS-29 and ADAMTS-20 as a distinct ADAMTS subfamily related to Caenorhabditis elegans GON-1."; J. Biol. Chem. 278:9503-9513(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: The precursor is cleaved by a furin endopeptidase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-- SIMILARITY: Belongs to peptidase family NL2B.
-- SIMILARITY: Contains 1 disintegrin-like domain.
-- SIMILARITY: Contains 1 GON domain.
-- SIMILARITY: Contains 15 TSP type-1 domains.
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SWART; SW00209; TSP1, 12.
PROSTIE: PSS0012; ADAM MERC) 1.
PROSITE: PS00427; DISINIEGRIN 1; FALSE NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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EMBL; AJ515153; CAD56159.3; -.
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LTADASFLAAGYTEVHLGTPERGAWESDAGPSDLRHCFYRGQVNSQEDYKA-VVSLCGGL 151
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                                                                         122 LHVLTQYDLVSAYEVDHRGDYVSHEIMHQRRRRAVAVSEVESL--HLRLKGPRHDFHMD
                                                                                                            180 LRTSSSLVAPGFIVQTLGKTGTKSVQT-LPPEDF--CFYQGSLRSHRNSPSHGGKFCEGS
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30-MS7_2000 (Red. 1.39, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2013 (Rel. 41, Last annocation update)
ADAMTS-1 precursor (RC 3.4.24.2) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS).
                                Conservative 151; Mismatches 327; Indels 149;
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        Best Local Similarity
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THDICVQGQCM -> SYNIDCNCVLK (in isoform
PROSITE; PSS0214; DISINTEGRIN_2; FALSE_NEG.
PROSITE; PSS0003. TSP1, 12.
PROSITE; PS00142; ZINC, PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Alternative splicing.
21 PROPER
22 253 BY SIMILARITY.
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-!-INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY INTERLEMENTAL, OR IN VIVO IN KINREY AND HEART BY LIPOPOLYGACCHARIDE. ALGO INDUCED BY LI STIMULATION IN GRANULOSA CELLS OF PRECOVULATORY FOLLICLES.
-!-DOMAIN "HE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE BETRACELLULAR MATRIX.
-!-PHY THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
-!-SIMILARITY: Belongs to peptidase family M12B.
-!-SIMILARITY: Conteains I distinegran-like domain.
-!-SIMILARITY: CONTEAINS I TSP LYPE-1 domains.
-!-CANTION: REF. 2 SEDGENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION?
                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene.", 7. Biol. Chem. 272:556-562(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cathepsin i proceases.";
Proc. Natl. Acad. Sci. U.S.A. 97.4689-4694 (2000).
Proc. Natl. Acad. Sci. U.S.A. 97.4689-4694 (2000).
INCOTION: CLEANES AGGRECAN, A CARTILAGE PROTECCLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOROPERASE, MICH MAY BE ASSCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL, AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN POLLICULAR RUPTURE (BY
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-!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Progesterone-regulated genes in the ovulation process: ADAMTS-1 and
                                                                                                                                                                                              "The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gene encoding an ADAM family protein with TSP motifs."; Genomics 46:466-471(1997).
ADAMTSI.
Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20243757; PubMed=10781075;
Robker K. Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20389568; PubMed-10930576;
Kino K. Okada Y. Kawashima H., Nakamura H., Miyasaka M.,
Ohno H. Matsushima K.;
                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
MEDUIRE-97150761: PubMed-8995297;
Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura P.,
Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan."; FEBS Lett. 478:241-245(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION, AND MUTAGENESIS OF GLU-403.
                                                                                                                                                                MEDLINE=98110583; PubMed=9441751;
Kuno K., Lizasa H., Ohno S., Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extracellular matrix.";
J. Biol. Chem. 274:18821-18826(1999)
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                                                                         NCBI_TaxID=10090;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 167 LRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSVQTLPPED---FCFYQGSLRSHR 223 224 NSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEA 283 140 -----VGSAAALSLCEG----- 157 284 DICKLYCIAEGFDFFFS .---LSNKVKDGTPCSEDSRN-------VCIDG 322 323 ICELSVVSTSAHMPQ------PPKEDLFILPDBYKSCLRHKRSLLRSHRNEELN 370 208 VMDDETLPTSDSRPESQNTRNQMPVRDPTPQDAG--KPSGPGSIRKKRFV----SSPRY 260 19.5%; Score 1022.5; DB 1; Length 968; 30.6%; Pred. No. 1.2e-66; 1ve 99; Mismatches 319; Indels 185; Gaps R MEROPS; M12.221.

R MGD; M21.222.

R MGD; M31.222.

R MGD; M31.222.

R InterPro; JPR00166; AbAM.cyteine.

R InterPro; JPR00166; Disintegrin.

R InterPro; JPR00166; Disintegrin.

R InterPro; JPR001694; TSP1.

R InterPro; JPR001695; RepEnJysin.

R InterPro; JPR001695; RepEnJysin.

R InterPro; JPR001695; RepEnJysin.

R InterPro; JPR001695; RepEnJysin.

R Pfam; PP01695; PP0 M12E, Dropep. 1.

R Pfam; PP01695; RepEnJ; RepEnJ; SPP1.

R PR0171; PP01695; RepEnJ; SPP1.

R SWART; SW00169; TSP1.

R SWART; SW00169; TSP1.

R SWART; SW00169; TSP1.

R SWART; SW00169; TSP1.

R SWART; SW00199; TSP1.

R RROSITE; PS00142; DISINTEGRIN.

R PROSITE; PS00142; ZINC PR0TEABE; I.

M RYCALGAE; MECALLORYCEASE; ZINC PROTECTIO: SIGNAL

R PROSITE; PS00142; ZINC PR0TEABE; I.

M RPCATGAE; PSCO144; AND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION: STAND PROTECTION PROTECTION PROTECTION PROTECTI N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL) (BY SIMILARITY). (BY SIMILARITY). CYSTEINE SWITCH (POTENTIAL) 105841 MW; 42EBDA55499FB6C1 CRC64; E->Q: LOSS OF ACTIVITY. N -> S (IN REF. 2). T -> S (IN REF. 2). DISINTEGRIN-LIKE, TSP TYPE-1 1. ZINC (CATALYTIC) ZINC (CATALYTIC) (CATALYTIC) METALLOPROTEASE ISP TYPE-1 2. TSP TYPE-1 3. CYS-RICH. ADAMTS-1 POLY-ARG EMBL; AB001735; BAA24501.1; ALT INIT. EMBL; D67076; BAA11088.1; ALT_FRAME. SPACER 266; Conservative 968 476 559 615 725 850 403 425 4 968 AA; Local Similarity ACT SITE METAL MUTAGEN CONFLICT CONFLICT CARBOHYD TARBOHYD CARBOHYD CARBOHYD SEQUENCE Query Match CHAIN DOMAIN DOMAIN DOMAIN DOMAIN STAL Matches Š 絽 ð 셤 à 유 ö 윱 ò This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

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495 EESKHC -- PDAASTCTTLWC -- TGTSGGLIVCQTKHFPWADGTSCGEGKWCVSGKCVNKT 550
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                                              146 GMCSKYRSCTINEDIGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG----NIMSPTLA 500
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261 VETMLVADQSMADFHG-SGLKHYLLTLFSVAARFYKHPSIRNSISLVVVKILVIYBEQKG 319
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16-COT-2001 (Rel. 40, Created)
16-COT-2001 (Rel. 40, Last sequence update)
28-TBB-2003 (Rel. 41, Last annocation update)
ADAMTS-1 precursor (EC 3.4.24.) (A disintegrin and metalloproteinase
with thrombospordin motifs 1) (ADAM-TS 1) (ADAM-TS 1)
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Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens J.A.,
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Rokarryce, Pteravoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Monmalia; Butheria, Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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BUDINE-20204099; PubMed-10847466;

Diamantis I., Luethi M., Hoesli M., Reichen J.;

"Cloning of the rat ADAMTS-1 gene and its down regulation in

endothelial cells in cirrhotic rats.";

Liver 20:165-177(2000).
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Little S.P., The disintegrin and metalloprotease with the
"Induction of a disintegrin and metalloprotease with the
thrombospondin rype I morif (ADAMTS)", Johnson Stephenses, Stephented (MAX-1999) to the EMBL/Genfank/DebU databases.
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                                                                                                                                                                                                                                                                                                            CTRRHOTIC LIVER.
--- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRAGELULIAR MATRIX.
--- PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLORD IN ITS TURNOVER, HAS ANGIOGRADIC INHIBATIOR ACTUVITY (BY SIMILARITY). ACTUVE METALLORDCIANSE, MINCH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHERIA, MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
                                                                                                                                                       CRANATIC ACTIVITY: Cleaves aggrecan at the 1683-Glu-|-Leu-1684 site, within the chondroltin sulfate attachment domain. CORACTOR: Binds 1 zinc ion per submit (By similarity). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
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I -y V (IN REF. 2).

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PROSITE; PSSG214; DISINFRERIN 1; PALSE NEG.
PROSITE; PSSG0214; DISINFRERIN 2; PALSE NEG.
PROSITE; PSSG0124; ZINC_PROTEASE, 1.
PROSITE; PSSG0027; TSP1, 3.
HACKITE; PSSG0027; TSP1, 3.
HACKITE; PSG0027; TSP1, 3.
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REPROSITE; PSP1, 3.
REPROSITE; PSP1, 3
                                                                                                                                                                                                                                                                   matrix (By similarity).
INDUCTION: DOWN-REGULATED IN ENDOTHELIAL CELLS DERIVED FROM
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SIMILARITY: Belongs to peptidase family M12B.
-:- SIMILARITY: Contains 1 disintegrin-like domain.
-: SIMILARITY: Contains 3 75P type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METALLOPROTEASE.
DISINTEGRIN-LIKE.
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TSP TYPE-1 3.
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InterPro; IPRO06586; ADAM cysteine.
InterPro; IPR001765; Disintegrin.
InterPro; IPR001765; Disintegrin.
InterPro; IPR001894; TGP1.
InterPro; IPR000894; TGP1.
InterPro; IPR000894; TGP1.
InterPro; IPR0008025; Zn. Wirpeptdse.
Pfam; PF01421; ReprojVsin; 1.
Pfam; PF01421; ReprojVsin; 1.
SMART; SW00809; TSP1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF149118; AAD34012.1; -. EMBL; AF304446; AAG29823.1; -.
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                                                                                                             15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADAWTS-19 precursor (EC 3 4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 19) (ADAW-TS 19) (ADAW-TS19).
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                             Lopez-Otin C.; "Cloning, expression analysis, and structural characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0427; DISINTEGEIN 1; FALSE NEG.
PROSITE; PSO0427; DISINTEGEIN 2; FALSE NEG.
PROSITE; PSO0042; TSP1; S.
PROSITE; PSO0142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: The precursor is cleaved by a furin endopeptidase (By similarity)
-!- SIMILARITY: Belongs to peptidase family M12B.
-!- SIMILARITY: Contains 1 disintegrin-like domain.
-!- SIMILARITY: Contains 1 PLAC domain.
-!- SIMILARITY: Contains 5 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                         seven novel human ADAMTSS, a family of metalloproteinases with disincegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM, 60513; ...
MIM, 60513; ...
MIM, 60513; ...
MILERPO, 1PRO0250; PED, N12B, propep.
InterPro; 1PRO001590; Reprolysin.
InterPro; 1PR000684, TSP1.
InterPro; 1PR000684, TSP1.
InterPro; 1PR000684, TSP1.
InterPro; 1PR006025; Zn. WTpeptdee.
Pfam, PP01421, Reprolysin; 1.
Pfam, PP01421, Reprolysin; 1.
Pfam, PP01421, Reprolysin; 1.
Pfam, PP01421, Reprolysin; 1.
PR08TF; SM02029; TSP1; S.
PROSITE; PS50215; ADAM_WERRO; 1.
PROSITE; PS00546; CKSTEINE_SWICH; FALSE_NBG.
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ADAMTS-19.
METALLOPROTEASE.
DISINTEGRIN-LIKE.
                                                                PRT; 1207 AA
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                15-SEP-2003 (Rel. 42, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Extracellular matrix.
                                                                STANDARD;
                                                                                                                                                                                               Homo sapiens (Human)
                                                              AT19 HUMAN
Q8TE59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826 RNALRRYYLNGHWIVDWPGR-YKFSGTIFDYRRSYNEPENLIATGPINETLIVELLFQGR 884
                                                                                                                                                                                                                                                              80 LRIDAFGQQLHIKLQPDSGFLAPGFTLQTVGRSPGSEAQHLDPTGDLAHCFYSGTV---N 136
                                                                                                                                                                                                                                                                                                                               284 DICKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDL 343
                                                                                                                                                                                                                                                                                                                                                                                             157 -----LQGEEPF-----183
                                                                                                                                                                                                                                                                                                                                                                                                                              344 FILPDEYKSCLRHKR......SLLRSHRNBELN........370
                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 SIAPPRFHILRRRRRGSGGAKCGVMDEETLPTSNSGRESQNIPDQWPLRNPTPQGAGKPT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------DGLMGKDGTRHDHAILLTGLDIC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 SWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKK 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 G--SHTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHBLGHVFNMPHD-DAKHCAS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRK-----CETKFMPAAEGTI 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 PGTLYDANRQCQFTFGEESTHC--PDAASTCSTLWC--TGTSGGLLVCQTKHFPWADGTS 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 GGKYCEGKRVRYRSCNIEDCPDNNGKTFREEQCEAHNEFSKASFGNEPTVEWTPKYAGVS 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DODLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDV 771
                                                                                                                                                                                                                                167 LRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSVQTLPPED---FCFYQGSLRSHR 223
                                                                                                                                                                                                                                                                                            224 NSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGKFCEGSTRTLKLCNSQKCP-RDSVDFRAAQCABHN--SRRFRGRH--YKWKP-YTQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VETLVVVDKKMMQNHGHENITTYVLTILNMVSALFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 SEG-----NIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 FNGVSGDSHLMASMLSSLDHSOPWSPCSAYMVTSFLDNGHGECLMD--KPONPIKLPSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 CGHDMWCRGGQCVKYGD--EGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 CGEGKWCVSGKCVNKTDMKHFATPVHGSWGPWGPWGDCSRTCGGGVQYTWRECDNPVPKN
                                                                                                                                                                                 1.4e-66;
hes 304; Indels 221; Gaps
                                                                                                                                                                 19.5%; Score 1021.5; DB 1; Length 967; 30.3%; Pred. No. 1.4e-66; ive 93; Mismatches 304; Indels 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NPGVAWEYSMPRIGTEKQPP--AQPSYT-WAIVR-SECSVSCGGG 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 ALRPKIKYTYFWKK----KTEPFNAIPTFSEWVIEEWGECSKTCGSG 973
                                                                                                                                   105705 MW; F93C864F6DCDB4CF CRC64;
V -> A (IN REF. 2).
E -> TR (IN REF. 2).
E -> TR (IN REF. 2).
THY -> NLIKE (IN REF. 2).
THY -> NLIKE (IN REF. 2).
S -> F (IN REF. 2).
L -> V (IN REF. 2).
I -> T (IN REF. 2).
                                                                                                                                                                                 al Similarity 30.3
269; Conservative
      49
72
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967 AA;
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862 PENLIATGPTNETL-IVELLFOCRNECVAMEYSMPRLC	anino-propegiate processing enzyme) (Procollagen II N-proceinase) (PC 11-PF)  BY ADANTSI OK KIAAO366.  BOANTSI OK KIAAO366.  MURLTARID-506671   Primates; Catarrhini; Hominidae; Homo.  MURLTARID-50667212   PubMed-11008482.  MURLTARID-50667212   PubMed-11008482.  MURLTARID-506671   PubMed-11008482.  MURLTARID-506671   PubMed-11008482.  MURLTARID-506671   PubMed-11008482.  MURLTARID-506671   PubMed-11008482.  MURLTARID-506671   PubMed-11008482.  MURLTARID-506871   PubMed-11008482.  MURLTARID-506871   PubMed-11008482.  MURLTARID-506871   PubMed-11008482.  MURLTARID-506871   PubMed-1100842.  MURLTARID-506871   PubMed-1100842.  MURLTARID-506871   PubMed-1100842.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARID-506871   PubMed-1100872.  MURLTARITY: Contains 1 disinegrin-11se domain.  MURLTARITY: Contains 1 disinegrin-11se domain.  MURLTARITY: Contains 1 disinegrin-11se domain.  MURLTARITY: Contains 1 disinegrin-11se and the EMBLO ON Commercial on the Empoyen Biodifformatics and the Emblore of Exercice on the Empoyen Biodifformatics and Commercial on the Empoyen Biodifformatics and Commercial on the Empoyen Biodifformatics and Commercial on the Empoyen Biodifformatics allong as the content is in no centure of commercial on centurines requires allong as expendent to centure and employed an employed and employed and expendent memail to license allong	EMBL, AF247668; AAX28400.1; EMBL, AB022364; BAA20821.1; MEROPS, M12.220; Genew; HGNC:219; ADAWTS3.
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975 10037 10083 10083 1195 2216 2216 482 483 486 486 486 797 949 949 797 797 797 797	Similarity 31.7%; Pred. No. 3.1e-66; Conservative 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 110; Mismatches 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependentale 296 Lirlependent	GYQSLDICANGRCQKVGCDGLLGSLAREDHCGYCNGNG VTI PSGARSIRIYEMNYSTSYISVRNALRRYYLNGHWT :   :    ::   LVIPAGARRIKVVEEKPAHSYLALRDA-GKQSINSDWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557
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                                                                412 ------KDGTRHDHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRS 453
                                                                                                           630 SSWSPCSRICGGGVSHRSRLCINPKPSHGGKFCEGSIRTLKLCNSQKCPRDSVDFRAAQC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748 VCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHNVTIPSG 807
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                                                                                                                                                                                                         454 CTINEDIGLGLAFTIAHESGHNFGMIHDGEGNMC--KKSEGNIMSPTLAGRNGVFSWSPC 511
                                                                                                                                                                                                                                                                                                                                             512 SRQYLHKFLSTAQAICLADOPKPVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690 AEHNSR-RFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCS-EDSRN 747
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15-5EP-2003 (Rel. 42, Last Sequence update)
15-5EP-2003 (Rel. 42, Last Sequence update)
ADAMTS 19 precursor (EC 3. 4.4.4.1) (A distincegrin and metalloproteinase
with thrombospondin motifs 19) (ADAM-TS 19) (ADAM-TS19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499 FDPCKQLWCSHPDNPYFCKTKKGPPLDGTECAAGKWCYKGHCM-WKNANQOKQDGNWGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 KDICKALWCHRIGRK--CETKFMPAAECTICGHDMWCRGGOCVKYGDEGPKPTHGHWSDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 EAGNHRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYVSHEIMHQRRRRAVAV-SEV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTLPPEDPCFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNSQKC--PRDSVDFRAAQCAE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 KTEPLQTNCAYVGDIVDIPGT-SVAISNCDGLAGMIKSDNEEYFIEPLE----RGKQMEE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 HNSRRFRGRH--YKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 DGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNE-ELNVETLVVVDK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 EKGR----IHVVYKRSAVEQAPIDMSK-----DPHYRESD-----L 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAGNEEMVQIDLPIKR----YREYELVIPVSTNLEGRYLSHILSASHKKRSARDVSSNP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS501032; TSP1, 4.
PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
REPEA! SKREAILOPING MEATIX, HEGBAIL-DINDING.
REPEA!, EXTRACELLULAR MARTIX, HEGBAIL-DINDING.
SIGNAL.
2 SIGNAL.
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.
SINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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    GO; GO:0005578; C:extracellular matrix; NAS. GO; GO:000578; C:extracellular matrix; NAS. GO; GO:000272; Francallo-obediase activity; NAS. GO; GO:000270; F:zinc ton binding activity; NAS. GO; GO:000574; F:collagen catabolism; NAS. GO; GO:000574; F:collagen catabolism; NAS. Incerpro; PR00195; P:collagen fibril organization; NAS. Incerpro; PR00195; P:collagen fibril organization; NAS. Incerpro; PR001897; P:collagen fibril organization; NAS. Incerpro; PR001897; P:collagen fibril organization; NAS. Incerpro; PR001897; P:collagen fibril organization; NAS. Incerpro; PR001897; P:collagen fibril organization; PEGM: PEGM: Reprolysin; O:collagen fibril organization; PEGM: Reprolysin; O:collagen fibril organization; PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: PEGM: 
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BY SIMILARITY.
ADAWTS-3.
METALLOPROTEASE.
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TSP TYPE-1 3.
TSP TYPE-1 4.
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                                        YQGSLRSHRNSPSH-----GG------KFCEGSTRTIKLCNSQKCPRDSVDFRAA 258
                                                                                                                                                                                                                       C------GVISDKGR----PRS-------KKIADNRREKRYSYKLSQEYNIETVVVA 336
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DPAMVSYHGADAARRFILTILNMVFNLFQHKSLGVQVNLRVLKLILLHETPADLYIGHHG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG-NIMS-PTL 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854 DYRRSYNEPENLIATGPINETL-IVELLFQGRNPGVAWEYSMPRLGTEKQPPAQ----- 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    862 HYLRR-GLWEXISAKGPTTTPLHLJAVLLFQDQNYGLHYEYTVP---SDPLPDNQSKEPG 917
  ----ILRIPALSRDLYLLLRRDGRFLAQRFAVEQWPKPGPDPTRATADPGSSLLPDASCF
                                                                              225 YTGTVLRHPGSLASFSTCGGGLMGFIQLNEDFLFIEPFNDTMAIIG------
                                                                                                                 QCAEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNV
                                                                                                                                                       ----BPHRLYROKR----TENSAVHRHH
                                                                                                                                                                                                CIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRSHR-NEELNVETLVVVV
                                                                                                                                                                                                                                                                                                                                                       -----GKDGTRHDHAILLTGLDICSWKNEPCDTLGF
                                                                                                                                                                                                                                                                                                                                                                               397 EKMLESFCKWQHEEFGRRNDVHLEMSTSWGEDIAAVDAALLITRKDFCVHKDEPCDTVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFGEKAKLCMLDFKKDICKALWCHRIGR-KCETKFMPAAEGTICGHDMWCRGGQCVKYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 LFGPLASFCQ-EMQHVICTGLWCKVEGEAECRIKLDPPMDGTDCDPGKWCKAGECTR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 OKCPRDSVDFRAAQCAEHNSRRFRGRH-YKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 PPCPAGLPGFRDWQCQAYSVRISYPKHALQWQ--AVFDEEKPCALFCSPVGKEQPVLLSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 RGACYVEVLVIPAGARRIKVVEEKPAHSFLALRDASKQ-SINSDWKIEHSGAFSLAGTTV
                                                                                                                                                                                                                                                                           DKKMMQNHGHENITTYVLTILNMVSALFKDGLM-------
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAMTS.17 precursor (EC 3.4.24.-) (A disintegrin and metalloprotei)
with thrombospondin motifs 17) (ADAM-TS 17) (ADAM-TS.17)
BOMMTS.17
BUARYOCE, Meszoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarthini, Hominidae, Homo.
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALSSGTPASWOPPLPPQRPSSPPPAQQEEPSAEEV------168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POEBATRGOSEPWFGSPL------EPGAEDEBELESQBLPRGSSG-----DT
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N-LINEED (GLCNAC.) (POTENTIAL).
N-LINEED (GLCNAC.) (POTENTIAL).
N-LINEED (GLCNAC.) (POTENTIAL).
N-LINEED (GLCNAC.) (POTENTIAL).
N-LINEED (GLCNAC.) (POTENTIAL).
           similarity.

SIMILARITY: Belongs to peptidase family M128.

SIMILARITY: Contains 1 disintegrin-like domain.

SIMILARITY: Contains 5 TSP type-1 domains.

CAUTION: By homology with the human sequence, it is uncertain whether Met-1 or Met-5 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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larity 28.4%; Pred. No. 4.3=64;
Conservative 133; Mismatches 362; Indels 250;
precursor is cleaved by a furin endopeptidase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134560 MW; 0AB812ABAB4BB7A2 CRC64;
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PROSITE; PS5015, ADAM MEDRO, 1.
PROSITE; PS00546; CYSTEINE SMITCH; FALSE NEG.
PROSITE; PS00214; DISINTEGRIN 2; FALSE NEG.
PROSITE; PS50092; TSP1, 5.
PROSITE; PS00125; ZINC, FROTEAGE; 1.
PAGTCLASE; PS01125; ZINC, FROTEAGE; 1.
RYGYCLASE; Metalloprotease; Zinc; Signal; Glyc.
Repeat; Extracellular matrix.
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TYPE-1 1.
CYS-RICH.
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ADAMTS-19,
METALLOPROTEASE.
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CYSTEINE SWITCH
ZINC (CATALYTIC)
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TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
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                                                                                                                                                                                                                                                                                  EMBL; AVISE183; AAN10155.1; -. MGD; MGI:2442875; AAN10155.1; -. SWART; SMO668; ACR; 1. SWART; SMO209; TSP1; 5.
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1210 AA;
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135 ------PGSLVSLSACGAAGGLVGLIQLGQEQV---LIQPLNNSQGPFSGREHLIRR 182
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                                                                Query Match
18.8%; Score 965; DB 1; Length 1095;
Beet Local Similarity 30.1%; Pered. No. 75-6-4;
Mackhes 259; Conservative 103; Mismatches 281; Indels 212; Gape
839 839 N-LINKED (GLCNAC. . .) (POTENTIAL) 894 894 N-LINKED (GLCNAC. . .) (POTENTIAL) 1095 AA; 121099 MW; ASC6540484754D5D CRC64;
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                                                                                                                                                  -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                  Lopez-Otin C., "Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
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PROSITE; PS50012; TSP1; S.
PROSITE; PS00142; ZINC_PROTBASE; 1.
PROSITE; PS01042; ZINC_PROTBASE; 1.
Repeat; Extracellular matrix.
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BY SIMILARITY.
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       [1]
SEQUENCE FROM N.A.
MEDINE-21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                        -:- SIMILARITY: Belongs to peptidase family M12B.
-:- STMILARITY: Contains 1 distinceptin-like domain.
-: SIMILARITY: Contains 1 TSP type-1 domains.
-: SIMILARITY: Contains 5 TSP type-1 domains.
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TSP TYPE-1 1.
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PROSITE, PSSOS46, CYSTELME SMITCH: FALSE NEG.
PROSITE, PSOO427; DISTATEGRIN 1: FALSE NEG.
PROSITE; PSSO214; DISTATEGRIN 2: FALSE NEG.
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ADAMTS-17.
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TSP TYPE-1 4.
TSP TYPE-1 4.
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InterPro, 187001590, Reprolysin.
InterPro, 187001590, Reprolysin.
InterPro, 187001693, ISB,
InterPro, 187001603, ISB,
InterPro, 187001603, ISB,
InterPro, 187001603, ISB,
Pfam, PRO1421, Reprolysin; ISB,
Pfam, PRO0401, 18P, 15
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MEROPS; M12.222; -Genew; HGNC.217; ADAMTS1.
MIM; 605174; -
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"Prediction of the coding sequences of unidentified human genes. XVI.
The complete sequences of 150 new cDNA clones from brain which code
for large proceins in vitro.";
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30-MAX-2000 (Rel. 39, Created)
16-CT-2010 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last samotration update)
16-SEP-2003 (Rel. 42, Last amotration update)
18-MAMTS-1 precursor (EC 3.4.24. 9) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).
                                                                                                                                      SQUBNCE FRICH A.A. Berivill X., Arbones M.L.; Casas C. Pritchest M.A., Estivill X., Arbones M.L.; Casas C. Pritchization and mapping on human chromosome 21 of the worthologue of murine Admirs-1. Submitted (JUL.1999) to the EMBL/Genbank/DDBJ databases.
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20247184; PubMed=10785405;
Glienke J., Schmatt A.O., Pilarsky C., Hinzmann B., Weiss B.,
Rosenthal A., Thierauch K.H.;
"Differential gene expression by endothelial cells in distinct
                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem. 267:2820-2830(2000).
                                                                                                                                                                                                                                         MEDLINE=99367466; PubMed=10438512;
                                                                                                                                                                                                               SEQUENCE FROM N.A., AND FUNCTION.
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TISSUE=Endothelial cells;
                                                                         Homo sapiens (Human)
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                                                        -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
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GO; GO:008285; P:negarive regulation of cell proliferation; TAS.
InterPro; IRROGES86; ADAM cysteine
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Repeat, Extracellular matrix, Heparin-binding.
SIGNAL
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P -> A (IN REF 4 AND 5).
C -> H (IN REF 1).
S -> N (IN REF 1).
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                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: Belongs to peptidase family M12B.
-i- SIMILARITY: Contains 1 disintegrin-like domain.
-i- SIMILARITY: Contains 3 7SP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | InterPro. | IRRN01763 | Disintegrin. |
| InterPro. | IRRN01763 | Disintegrin. |
| InterPro. | IRRN01801 | Reprolysin. |
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| InterPro. | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01801 | IRRN01
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TSP TYPE-1 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF060152; AAD48080.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF207664, AAF23772.1, -.-
EMBL, ABO37767, BAA52864.1, ALT_INIT.
EMBL, AP001697, BAA5562.1, -.-
EMBL, AL162080, CAB82413.1, -.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105383 MW;
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Score 984.5; DB 1; Length 967;

18.8%;

Query Match

Occal Similarity 30.9%; Pred. No. 7e-64; es 270; Conservative 104; Mismatches 328; Indels 173; Gaps 35;	:	60 LVVPELERAPGHGTTRLRLHAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPE 117	210 EDFCFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEH 263	IS IDEANCFIGGIVNGDFGGAA-ABSECEGVAGATIDEGEAIFIQFEFAASEABAFABET	264 NSRRFRGRHYKWRFYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTFCSEDSRNVCIDGI 323	26 TO STANDARD THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRAN	CELONYOLDERPROPERSAGE   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELONYOLDER   CELO	-	:     ;     ;    ;    ;    ;    ;    ;	407 DGLMGKDGTRHDHAILLIGEDICSWKNEP 435	309 ILVIHDEQKGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQT 366	436 CDTLGFAPISGWCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG 492	367 CDTLGMADVGTVCDPSRSCSVIEDDGLGAAFTTAHELGHVFNMPHD-DAKQCASLNGVNQ 425	493NIMSPTLAGRNGVFSNSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYD 550	426 DSHWMASWLSNLDHSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYD 483	551 ANTQCKWQPGEXAKLCMLDFKKDLCKALWCHRIGRKCETKFWPAABGTICGHDMW 605	484 ANROCOFTEGEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKM 539	606 CRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCB 663	540 CINGKCVNKTDRKHFDTPFHGSWGWMGPWGDCSRTCGGGVQYTWRECDNPVPKNGGKYCE 599	664 GSTRTLKLCNSQKCP-RDSVDFRAAQCAEHNSRRFRGRHYKWKP-YTQVEDQDLCK 117	600 GKRVRYRSCNLEDCPDNNGKTFREEQCEAHNEFSKASFGSCPAVEWIPKYAGVSFKDRCK 659	718 LYCIAEGFDFFFSLSNKVKDGTPCSEDGRNVCIDGICERVGCDNVLGSDAVEDVCGVCNG 777	660 LICQAKGIGYFFVLQPRVVVGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDXCGVCGG 719	778 NASACTIHRGLYTKHHHTNQYYHNVTIPSGARSIRIYEMNVSTSYISVRNALRRY 832	720 NGSICKKISGSVTGAKPGYHDIIIIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTY 777	833 YLNGHWTVDWPGR-YKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVA 889	778 ILNGDYTLSTLEQDIMYKGVVLRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRFKIK 837	890 WEYSMPRIGTEKQPPAQPSYT-WAIVR-SECSUSC 922	838 YTYFVKKKKESFNAIPTFSAMVIEEMGECKSC 870	
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Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
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23:23:19 ; Search time 76 Seconds	(without alignments)	3232.448 Million cell updates/sec
2003,		
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Title: Perfect score: Sequence:	US-09-981-151A-8 5236 I MKPRARGWRGLAALMWLLAQLEAACQPSATAYTALAFLES 952
Scoring table:	BLOSUM62 Gapop 10.0 , Gapexc 0.5
Searched:	830525 seqs, 258052604 residues
Total number of	Total number of hits satisfying chosen parameters: 830525
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8te57 homo sapien	Q8k206 mus musculu	Q8ive2 homo sapien	Q8te60 homo sapien	Q8bkal mus musculu	Q8bky1 mus musculu	Q8cg28 mus musculu	Q9w493 drosophila	Q8te59 homo sapien	Q8ne26 homo sapien	Q19791 caenorhabdi	Q8hzm8 equus cabal	Q8bzdl mus musculu	Q8k384 mus musculu	Q8bnj2 mus musculu	Q8mrl5 drosophila
SUMMARIES	DI	Q8TE57	Q8K206	QBIVE2	QSTEGO	QBBKA1	QSBKY1	Q8CG28	Q9W493	Q8TE59	Q8NE26	019791	Q8HZM8	Q8BZD1	Q8K384	QBBNJ2	QBMRL5
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## ALIGNMENTS

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REBULT 1

OGTES7 PRELIMINARY; PRT; 1072 AA.

10 GRTES7

OGTES7 PRELIMINARY; PRT; 1072 AA.

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233 SRTWELAHQPLHSSDLRLGLP---QKQHFC-----GRRKKYMPQPPKEDLFILPDE 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 ICSWKMEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYTKHHHTMQYYHMVTIPSGARSIRIYEMWVSTSYISVRNALRRYYLNGHWTVDWPGRYK 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        848 FSGTTFDYRRSYNEPENLIATGPINETLIVELLFQGRNPGVAWEYSMPRLGTEKQPPAQP 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           811 FSGTTFDYRRSYNEPENLIAIGPINETLIVELLFQGRNPGVAWEYSMPRLGTEKQPPAQP 670
                                                                                                                                                61 PLFSAGICVRHGIRSGSAWEPERPASSSIRGAAGLDGKGRDMDEAGNHRSQQINTGTENQ 120
                                                                                                                                                                                                                         21 TLHVLTQYDLVSAYEVDHRGDYVSHEINHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL 180
                                                                                                                                                                                                                                              59 -----EYDLVSAYBVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL 112
                                                                                                                                                                                                                                                                                                   181 RTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL 240
                                                                                                                                                                                                                                                                                                                        241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKWKPYTQVEA-DLCKLYCI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 YKSCIRHKRSLIRSHRNEBLNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKD-- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GLMGKDGTRHDHAILLTGLD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            691 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 750
                                                                         1 MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS 60
                                                                                                           1 MKPRARGWRGLAALWMLLAQVAEQAP-----------ACAMG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 R-----TEEADYFLRPLPSHLSWKL-GRAAQGSSPSHVLYKRSTEPHAPGASEVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                               292 AEGFDPPPS--LSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGGVSHRSRLCTNPKPSHGGKPCEGSTR
                                         72; Indels 143; Gaps
73.7%; Score 3858.5; DB 4; Length 1072; 75.6%; Pred. No. 0;
                                                                                                                                                                                       32 PAAAA------PGSPSVPRPPPPAERPG-------WMEKG--
                                       24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908 SYTWAIVESECSVSCGGGR 926
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  Query Match
Best Local Similarity 75.6*
Matches 740; Conservative
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Query Match 64.9%; Score 3400; DB 11; Length 900;
Best Local Similarity 65.7%; Pred. No. 3.6e-294;
Matches 646; Conservative 64; Mismatches 109; Indels 164; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVAPGEIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 CVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQTLHVLTQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 YDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEV--ESLHLRLKGPRHDFHMDLRTSSS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 QKCPRDSVDFRAAQCAEHNSRRFR-----GRHYKWKPYTQVEA------DL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 CKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFI 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 ARPHLHHDNFHLGPSQKQHF-----CGRRKK-------YMPQPPNDDLYI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 LPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALF 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 ----TKDTDYFLKPLPPHLTSKLNRSAQGDSPSHVLYKRSTERQAPRENEVLMITRKRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 KDGTIGGNINIVIVGLILLEDEQPGLAISHHADHTLTSFCQWQSGLMGKDGTRHDHAILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 TGLDICSWKNEPCDTLGFAPISGWCSKYRSCTVNEDSGLGLAFTIAHESGHNFGWYHDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GLMGKDGTRHDHAILL
                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mypothetical protein.
Mys musculus (Mouse)
Bukaryota, Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muxidae; Muxinae; Mus.
                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0215; ADAM_MEPRO; 1.
PROSITE; PSS0037; TSP1; 1.
PROSIDE; PSS0037; TSP1; 1.
SEQUENCE 900 AA; 100679 MM; 590BE2B0E73740FF CRC64;
                                                                                                                                                                                                                                      EMBL, BC034739, AAH44739.1, -...
InterPro, IPR002870, Pep_M12B_propep.
InterPro, IPR001590, Reprolysin.
                                                                                                                                                                                                                                                                                                           Pfam: PF01562; Pep_M12B_propep; 1.
Pfam: PF01421; Reprolysin; 1.
Pfam: PF00090; tsp_1; 1.
SMART; SK00209; TSP_1; 1.
                                                                                                                                                                                                                                                                                              InterPro; IPR000884; TSP1.
PRELIMINARY;
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                                                                                                                                                     NCBI_TaxID=10090;
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592 YYLNGHWIYUDWPGRYKFSGTIFDYRRSYNBPBNLIATGPINETLIVBLUFPGRNPGVAME 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 HEIMHIGRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSV 204
532 PKPVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRKCETKF 591
                  292 PKPVKEYKYPEKLPGELYDANTQCKQQGGKAKLCMLDFKKDICKALMCHRIGRKCETKF 351
                                                                         651
                                                                                                                                                                         412 NPKPSHGGKFCBGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVE 471
                                                                                                                                                                                                                                                    772 CGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRR 831
                                                                                                                                                                                                                                                                                                                                                                                 832 YYLNGHWTVDWPGRYKFSGTTFDYRRSYNBPENLIATGPTNETLIVELLFQGRNPGVAWE 891
                                                                                                                                                    652 NPKPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVE 711
                                                                                                                                                                                                                             712 DODLCKLYCIARGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDV 771
                                                                                                                                                                                                                                                                                                                                         532 CGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRR 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 MPAAEGTICGHUMWCRGGQCVKYGDEGPRPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, expression analysis, and structural characterization of seven novel human ApAWTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).

BMEN, A3311903; CAC83612.1; -. Genew, HGMC:11710; ADAWTS.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.0%; Score 2408; DB 4; Length 1081; Best Local Similarity 51.0%; Pred. No. 1.7-205; Matches 463; Conservative 118; Mismatches 197; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21856482; PubMed=11867212;
A.S. Obaya A.J., Liamazares M., Garabaya C., Quesada V.,
Lopez-Orin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081 AA; 119655 MW; 0438BF645676461E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             892 YSMPRLGTEKOPPAQPSYTWAIVRSECSVSCGGR 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 YSMPRLGTEKQPPAQPSYTWAIVRSECSVSCGGGQ 686
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InterPro, IPR0015970, Reprolysin.
InterPro, IPR001599, Reprolysin.
Fram, PR00142, Pep M12E propep; 1.
Fram, PR00142, Reprolysin; 1.
Fram, PR001901, Esp. 1, 4.
RAMER, RW00209, TSB1, 4.
RR051TE, PS50021, FSB1, 4.
RR051TE, PS50021, PSP1, 3.
PR051TE, PS50021, PSP1, 3.
PR051TE, PS50021, PSP1, 3.
PR051TE, PS50021, PSP1, 3.
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ADAMTS18.
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                                                                                                                                                                                                                                                    334 HMPQPPKEDLFILPDBYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMQNHGHENITTY 393
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                         604 MWCRGGQCVKYGDEGPFKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCE 663
                                                                                                  664 GSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAE 723
                                                                                                                                                                           724 GPDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACT 783
                                                                                                                                                                                                                                                                                                                           844 GRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAWEYSMPRLGTEKQP 903
  544 LPGELYDANTQCKWQFGEXAKLCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTICGHD 603
                                                                                                                                                                                                                                                                                                        784 IHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Ohara O.;
"The rucleotide sequence of a long CDNA clone isolated from human.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB095949; BAC23125.1;
"Thy Chatical protein.
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01-MAR-2003 (TYEMBLEE). 23, Last Sequence update)
01-MAR-2003 (TYEMBLEE). 23, Last semectation update)
Hypothetical protein KIAA2029 (Fragment).
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Matches 397; Conservative
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261 AEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDG-----TPCSEDS 315
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                                                                                                                                                   316 R-----NVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSCLRHKRSLLRS 363
                                                                                                                                                                                                                                                                                                                   APISGMCSKYRSCTINEDIGLGLAFFIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAG 501
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                                                                                                               187 OEHNYSSPAG-HHPHVLYKRTAEEKIORYRGYPG-----SGRNYPGYSFSHIPHASOS
                                                                                                                                                                             239 RETEYHHRRLQKQHFC-----GRRKKYAPKPPTEDTYLRPDEYGSSGRPRRSAGKS
                                                                                                                                                                                                       364 HRNBELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDG-------
                                                                                                                                                                                                                                                              409 -----CSWKNEPCDTLGF
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical metalloprotease.
Wis musculus (Mouse)
Muschazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN-CSPEL/61; TISSUE=E9e;
MEDITE-2236681; Dubmed-113466851;
THE FARTON CONSORTION.
THE RANTON CONSORTION.
THE RIEM HOROME Exploration Research Group Phase I & II Team,
the RIEM Homome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,707 full-langth cDNss.";
MARCHE 420:563-573 (2002).
EMBL, AK053851; BAC35556.1; -.
Hypotherical Doceln.
120324 MW; BSF0395653536AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 DDARNV-----YAPKPPAEDAYLAFDEYGGTGRPRRSAGKSONG--LNVE
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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59.4%; Pred. No. 5.1e-192;
tive 90; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                              49 LPEYHIVSPVQVDAGGHVLSYGLHHPVTSSRKKRAAGGSG-DQLYYRISHEEKDLFFNLT 107
                                                                                                                                                                                                                                                                                                                                                                                                         182 TSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCPYQGSLRSHRNSPSHGGKFC----- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                      108 VNWEFLSNGYVVEK-------RYGNL-SHVKMVASSGQPCHLRGTVLQ 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 OGTTVGIGTAALSAC-----QGLTGFFHLPH 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 RHDHAILLIGLDICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGHN 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 HHDVAVLITRKDICAGVNRPCETLGLSQLSGMCQPHRSCNINEDSGLPLAFTIAHELGHS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 FGMIHDGEGNMCKK--SEGNIMSPTLAGRNGVPSWSPCSRQYLHKFLSTAQAICLADQPK 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 PVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRKCETKFMP 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 K-KGLKSNVIAPGVIYDVHHQČQLQYGPNATFC--QEVENVCQTLWCSVKG-FCRSKLDA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 AAEGTICGHDWWCRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNP 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 AADCIRCGEKKWCMAGKCIIVGKK-PESIPGGWGRWSPWSHCSRICGAGAGSAERLCNNP 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 KPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCABHNSRRFRGRHYKWKPYTQVEDQ 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 DLCKLYCIAEGFDFFFSLSNKVKDGTPCSE--DSRNVCIDGICERVGCDNVLGSDAVEDV 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 -- CELYCRPIDEQFSERMLEAVIDGTPCFEGGNSRNVCINGICKRVGCDYEIDSNATEDR 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 CGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNA-LR 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,710 full-length CDNAs.";
Nature 420:563-573(2002).
BYEUS, AKO46612; BAC33391.1;
NON TER 1009 1009 1009
SEQÜENCE 1009 AA, 113352 MW; 7B63218CFFE0FDB1 CRC64;
                                                                                                                                                                                                                                                                     Query Match 23.3%; Score 1218; DB 11; Length 1009; Best Local Similarity 32.8%; Pred. No. 2.5e-99; Matches 287; Conservative 130; Mismatches 307; Indels 152; Gaps
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                           STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 VSALFKDGLMGK------
Mus musculus (Mouse)
                                          NCBI_TaxID=10090;
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        SEQUENCE
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831 RYYLNGHWTVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFOGRNPGVAW 890
                                            357 KRSLLRSHRNEELNVETLVVVDXKMMQNHGHENITTYVLTILNMVSALFKDGLMG---- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 -----KDG-TRHDHAILLT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 LVTRLILLTEDQPTLEITHHAGKSLDSFCKWQKSIVSHSGHGNAIPENGVANHÖTAVLIT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 GLDICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAPTIAHESGHNFGMIHDGEG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 RYDICIYKNKPCGTLGLAPVGGMCERERSCSINEDIGLATAFITAHEIGHNFGMNDGVG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 NMC---KKSEGNIMSPILAGRNGVFSWSPCSRQYLHKFLSTAGAICLADOPKPVKEYKYP 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 NGCGARGODPAKLMANHITMKINPEVWSSCSRDYITSFLDSGLGLCLNNRP-PRODFVYP 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 BKLPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTIC- 600
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Estabhadite M., Nagarada R., Abe K.;
"Genomic Sentone Analysis in the Mouse t.complex Region.";
Submitted (NUL-2002) to the EMBL/Genbank/DDBJ databases.
EMBL, RES28163; AROLT300.1;
ERQUENCE 1070 AA, 117203 WW, 68996425EBAZBBDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                    891 EYSMPRIGIEKOPPAOPSYTWAIVR-SECSVSCGGG 925
                                                                                                                                                                                                                 813 EYTVRKDGLDND-VEKLLYFWQFGRWTECSVTCGTG 847
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Mus musculus (Mouse).
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SEQUENCE FROM N.A.
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RA Adams M D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M D., Celniker S.E., Li P.M., Hoskins R.A., Galle R.F.

RA Adams M D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Button G.G., Morreman J.R., Yandell M.D., Zhang Q., Chan L.X.,

Brandon R.C., Baxer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Addavania A., Baxendale J., Bayarakaracolu L., Beasley E.M.,

Ran K.H., Bernos P.V., Berman B.P., Blandari D., Bolshakov S.,

RA Borcova D., Botchan M.R., Bouck J. Brokstein P., Brottier P.,

RA Dercova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry S.M., Cawley S., Delloher A., Donel B.P., Blandari D., Bolshakov S.,

RA Cherry J.M., Cawley S., Delloher A., Donel S., Dunkov B.C., Dunn P.,

Ran Borcova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry S.M., Cawley S., Delloher A., Donel S., Dunkov B.C., Dunn P.,

Ran Borbin R.J., Bromes M., Dugan-Rocha S., Dunkov B.C.,

RA Durbin R.J., Bromes M., Dugan-Rocha S., Dunkov B.C.,

RA Harris N.L., Harvey D., Helman T.J., Hernander J.R., Rockfamm M.,

Randel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Harris N.L., Harvey D., Helman T.J., Hernander J.R., Rockfam M.,

Randel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Mannel B.E., Mollrosh T.C., Morleod M.P., Morberson D.,

RA Mount S.M., May M., Murphy B., Murphy L., Muzny D.M., Nalson M.,

Rander K., Siden K.A., Born S., Wobarry C., Worris J., Wang X.,

Rander K., Sardaling A.C., Turner R., Venter E., Sche H.,

Rander K., Starker S., Wang X.,

Rander K., Spier E., Spradling A.C., Turner R., Wenter E., Shen H.,

Rander K., Morges R., Rochel W., Saunders R., Wenter E., Spradling A.C., Turner R., Wenter E., Spradling A.C., Stapheron M., Stupsk, M., Shong S., Yao, Q.A.,

Rander K., Myessarman D.A., Weinstock G.M., Wang S., Wang S., Yao, Q.A.,

Rander K., Myessarman D.A., Weinstock G.M., Wang S., Wang S., Yao, Q.A.,

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Celniker S.B., Gocayne J.D., Amantaides P.G., Brandon R.C., Rogexs Y.,

Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Rerriers S., Dersett V., Doup L.E., Doyle C., Dresenek D., Farfan D.,

Ferriers S., Frise E., Galle R.F., Garg N.S., George R.A.,

Glognalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
                                                                                                                                                                                                                                                                       Bukarýota, Metazoá, Arthropoda, Héxapoda, Insecta, Pterygota, Propetera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydrovicela, Drosophilidae, Drosophila, Vell_nax1D=727;
               898 GIEKOPPAQPSYTWAIVR-SECSVSCGGGRCLPVLLLEAACQPSATA 943
                                             786 ARDALPP----YSWHYAPWTKCSAQCAGGSQVQVVECRNQLDSSAVA 828
                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                  PRT; 1059 AA.
                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                          CG4096 protein.
                                                                                                                                                    Q9W493;
                                                                                                                                     Q9W493
                                                                                                                                                                                                                                         CG4096
                                                                                                  RESULT 8
                                                                                                                      Q9W493
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138 HRGDYVSHEIMHHQRRRRAVAVSEVES----LHLRLKGPRHDFHMDLRTSSSLVAPGFIV 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 GAEVSNCGTRE-PRRRMETRLEWQARGKVKVQGGRQIRRHHHHHHHHHHKHKYRHHQQKI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 ----YETQFQTEPDHAEIPRRRRSI----SSPRHVETLIVADATM--SAFHRDLNGY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 BRHRRDLRTRSPLTTRHLNCHFHGKVRGQPATNVAISTCAGLVSCPNFCVLPELITLCQV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 ---PYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 HMPOPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMONHGHENITTY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 VLTILNMVSALFKDGLMG------ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 G--HIRTAGNEYFIEPSKEHEPHPVNGHPHVVFORSSVKPKHSLRKRNKRKRGGK--SGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.

Hradecky P., Hungy Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Tupy J.L., Bergman C., Berman B., Carlison J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,

Rashlurner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,

"Annotation of Drosophila melanogaster genome."
Pacleb J., Paragas V., Fark S., Patel S., Pfeiffer B., Phouamanavorg S., Pithman G.s., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Psequencing of Drosophila melanogaster genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 273; Conservative 132; Mismatches 309; Indels 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPRO60084; TSPI -/ InterPro; IPRO60084; TSPI -/ InterPro; IPRO60082, Zn Wirepctde.

PEam: PF01462; Pep W128_Dropep; I.

PEam: PF01421; RepCrivsin; I.

PEam: PF00090; Lep 1, 2.

PROSTER: PS02015; ADAW MEPRO; I.

PROSTER: PS02012; TSPI 2.

PROSTER: PS00142; ZINC_PROTEASE; I.

SEQUENCE 1059 AA; 113195 WM; AD3C99E47618F3D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLYBase, FEGIO029781, CG4096.
Interpro, IPR002870; Pep M128 propep.
InterPro, IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003435; AAF46065.2; -. HSSP; P15167; 1ATL. MEROPS; M12.231; -.
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636 AG---EWSLWGPCSRICSAGISSRERKC--PGLDSEARDCNGPRKQYRICENPPCPAGLP 690
                                                                                                                                                                                                                                                                                                                                                                            167 LRLKGPRHDFHMDLRTSSSLVAPGFIVQTL-----GKTGTKSV--QTLPPEDFCFYQGSL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 LRHPGSLASFSTCGGGLMGFIQLNEDFIFIEPLNDTMAITG--------H 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 NHGHENITTYVLTILNMVSALFKDGLM-------410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 FCKWOHEEFGKKNDIHLEMSINWGEDMISYDAALLITRKDFCVHKDEFCDIVGIAYLSGM 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 VFSWSPCSRQYLHKFLSTAQAICLAD-QPKPVKBYKYPEKLPGELYDANTQCKWQFGEKA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 DVSWSRCSKEDLERFLRSKASNCLLQTNPQSVNSVMVPSKLPGMTYTADEQCQ1LFGPLA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 KLCMLDFKKDICKALWCHRIGRK-CETKFMPAABGTICGHDMMCRGGQCVKYGDEGPKPT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578 SFCQ-EMQHVICTGL#CKVEGEKECRTKLDPPMDGTDCDLGKWCKAGECTS-RTSAPEHL 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 HGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGSTRTLKLCNSQKCPRDSV 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 DFRAAQCAEHNSRRFRGRH-YKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPC 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      691 GFRDWQCQAYSVRTSSPKHILQWQ--AVLDBEKPCALFCSPVGKEQPILLSEKVMDGTSC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                       167 LAIPAFSRDLYLLIRRDGRFLAPRFAVEORPNPGPFGPAGAASAPOPPAPPDAGCFYTGAV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 RSHRNSPSH----GGK-----FCEGSTRILKLCNSQKCPRDSVDFRAAQCAEH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 NSRRFRGRHYKWKPYTQVSADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 PHRVYROKRSMERKVTEKSA-LHSHYC---GI-----ISDK---GRP---RSRKIAESG- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 CELSVVSTSAMMPQPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 -----NIETVVVADPANUS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 CSKYRSCTINEDIGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG-NIMS-PTLAGRN-G 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 742 SEDSRNYCIDGICERYGCDNVLGSDAVEDYCGVCNGNNSACTIHRGLYTXHHHTNQYYHM 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        862 PENLIATGPINETL-IVELLFQGRNPGVAWEYS-----MPRLGTEKOPPAOPSYTWAIVR 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       866 WEKISAKGPTTAPLHILVILFQDQNYGLHYEYTIPSDPLPENQSSKAP--EPLFWMTHTS 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              802 VTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWIVDWPGRYKFSGTIFDYRRSYNE 861
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                                                                                                                                                                                                                                           Query Match

19.5%; Score 1018.5; DB 4; Length 1207;
Best Local Similarity 31.7%; Precd. No. 2.16-81;
Matches 270; Conservative III; Mismatches 296; Indels 175; Gaps
Pfam, PF00090; tsp_1; 5.
SMART; SM00209; TSP1, 5.
PROSITE; PS50215; ADAM MERRO; 1.
PROSITE; PS50022; TSP1, 5.
PROSITE; PS50028; ZINC_FUNSR_C2H2, 1, 1.
SPROSITE; PS00142; ZINC_FUNSR_C3H2, 1; 1.
SEQUENCE 1207 AA; 134061 MW; AP36F6BF5086FDE2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                884 YAIVRGNESNAGIFYZETILPALNV----TAGRQFQWRISNWTACSASCGGG----VOHRE 935
                               412 -----KDGTRHDHAILLTGLDICSWKNBPCDTLGFAPISGMCSKYRSCTINEDTGLGLAP 466
                                                                                                                                                                                                                                                                                                                         530 LGECLDDPPTPLDEYNYTGELPGMRYNARGQCRLQFNLTTDSEVGACSAPHEFCSTLWC- 588
                                                                                                                                                                                                                                                                                                                                                                                                               641
                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 KVNGECVTHMRPTAPGTLCGRNK#CQNGKCVR--RE5LAAVNGGWGWSEWSECSRSCGG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          762 VLGSDAVEDVÇGVCNGNNSACTIHRGLYTKHHHTNQ--YYHMVTIPSGARSIRIYEMNV$ 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 820 TSYISVR--NALRRYYLNGHWTVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIV 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         825 PHFLAIAIGDGGDRFYLNGDSLISMPGFFEIAGABSLYDR-VDEQETITIFQPIQHSISL 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           878 ELLFQGR--NPGVAWEYSMPRIGTEKQPPAQPSYTWAIVR-SECSVSCGGGRCLPVLLLE 934
                                                                                          413 NKGSEKDPHHHDVALLITRKNICA---NNCMTLGLANVGGMCKPKOSCSVNEDNGIMLSH 469
                                                                                                                                                            467 TIAHESCHNFGMIHDGEGNMCKKSEG---NIMSPTLAGRNGVFSWSPCSRQYLHKFLSTA 523
                                                                                                                                                                                                                   470 TITHELGHNFGMFHDTAKIGCHPRVGPIVHIMTPIFGADTLQVCWSNCSRKYITHFLDQG 529
                                                                                                                                                                                                                                                                                      524 QAICLADQPKPVKEYKYPEKLPGELYDANTQCKWQFG--EKAKLCMLDFKKDICKALWCH 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 GVSHRSRLCTNPKPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRH 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              702 YKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDN 761
                                                                                                                                                                                                                                                                                                                                                                                                           582 RIGRKCETKFMPAAEGIICGHDMWCRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765 IVDSEVQDDRCGVCGGSGDQCQPVRETYTDPPAAKDGAYVEIVTIPARARHILIRELANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T. "Cloping, expression analysis, and structural characterization of seven movel human ADAMTSS, a family of metalloproteinases with disintegrain and thrombospondin-1 domains.";

T. disintegrain and thrombospondin-1 domains.";

Gene 28:149-62(2007)

R. BMB1, AJ311904; CAC34565.1;

R. BMB1, AJ311904; CAC34565.1;

R. InterPro; IPR001509; PeprMT3B, propep.

R. InterPro; IPR001509; PeprOlysin.

R. InterPro; IPR007087; Znf C2H2.

R. InterPro; IPR007087; Znf C2H2.

R. InterPro; IPR007087; Znf C2H2.

R. InterPro; IPR007087; Znf C2H2.

R. InterPro; PR007087; Znf C2H2.

R. Fran; PF01421; Reprolysin; 1.
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Mammalia; Eutheria; Primates; Catarxhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE PROM N.A.
MEDLINB-21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
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01-JUN-2002 (TrEMBLrel, 21, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
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08TE59
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660 LICQAKGIGYPFVLQPKVVDGTPCSTDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGG 719
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                                                                                          606 CRGGQCVKYGDEG -- PKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCE 663
                                                                                                                                                                                                              664 GSTRILKLCNSQKCP-RDSVDFRAAQCAEHN----SRRFRGRHYKWKP-YIQVEDQDLCK 717
                                                                                                                                                                                                                                                                 600 GKRVRYRSCNLEDCPDNNGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCK 659
                                                                                                                                                                                                                                                                                                                               718 LYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                   778 NNSACTIHRGLYTKHHHTNOYYHMVTIPSGARSIRIYEMNV----STSYISVRNALRRY 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   833 YLNGHWIVDWPGR-YKFSGTTFDYRRSYNEPENLIATGPINETLIVELLFQGR--NPGVA 889
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Bonfield J., Burton J., Connell M., Copser T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copser T., Cooper J., Coulson A.,
Caxton M., Dear S., Du Z., Dutbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten T., Hillier L., Jier M., Johnston L.,
Lightning J., Lloyd C., Mcmarray A., Wortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Sauden R.,
Sanadon N., Santh A., Sonnhammer E., Staden R., Sultston J.,
Thierry-Meg J., Thomas K., Vaudin M., Paulpan K., Watterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabdiris elegans.
Bukaryota, Metazca, Nematoda; Chromadorea; Rhabdirida; Rhabditoidea;
Rhabditidae; Peidderihae; Caenorhabditis.
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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01-MOV-1996 (TERBELTE1. 01, Created)
01-NOV-1998 (TERBELTE1. 08, Last sequence update)
01-MAR-2003 (TERBELTE1. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838 YTYFVKK--KKESFNAIPTFSAWVIEEWGECSKSC 870
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InterPro; IPR001690, TSP1.
InterPro; IPR006084; TSP1.
Pfan: PF01421; Reprolysin; 1.
Pfan: PF00090; tsp_1; 14.
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MEDLINE=94150718; PubMed=7906398;
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EMBL, Z69361; CAA93287.1; JOINED.
HSSP, PL5167; LDTH.
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EMBL; Z69360; CAA93288.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 EDF--CFYQGSLRSHRNSPSHGGKFCEGSTRTLKLCNS----QKCPRDSVDFRAAQCAEH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 NSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 ...---KPPAPLQ.----VGGT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 C--GVVDDEPRPTGKAETEDEDEGTEGEDEGPOMSPODPALGGVGOPTGTGS-IRKKK-F 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 LRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFK-------406
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al Similarity 30.9%; Score 984.5; DB 4; Length 967;
al Similarity 30.9%; Pred: No. 1.6e-78;
270; Conservative 104; Mismatches 328; Indels 173; Gaps
                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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967 AA; 105387 MW; FF1D399674201C3D CRC64;
                                                                                                                           01-0CT-2002 (TERMBLEE) 22, Created)
01-0CT-2002 (TERMBLEE) 22, Last sequence update)
01-MAR-2003 (TERMBLEE) 23, Last sequence update)
Myportherical profesin.
Hyportherical profesin.
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Interpro; IRROUGOS, IN MYDeptdee.
Filam, Pro13c1, Pep Milb prope; 1.
Filam, Pro10121, Pep Milb prope; 1.
Filam, Pro10000, 150 1, 2.
SWART; SW00000, ACR 1.
SWART; SW00000, ACR 1.
SWART; SW00000, ACR 1.
PROSITE; PS001020; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
PROSITE; PS00102; TSP1, 3.
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InterPro, IPR006586; ADAM Cysteine.
InterPro, IPR001128; Cytodrome_B450.
InterPro, IPR003870; Pep M12B propep.
InterPro, IPR001590; RepZolysin.
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                                                                        PRELIMINARY;
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                  RESULT 10
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292 MYEYHG-RSLEDYVLTLFSTVASIYRHQSLRASINVVVVKLIVLKTENAGPRITQNAQOT 350
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                                                                                                                                                                                                                                                   180 LRT------SSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRS-HR 223
                                                                                                                                                                                                                                                                                                                                                              123 LHRWNQIPDSHNKSVPHFSNSNFAPMVLYLDSEEEVRGGMSRTDPD--CIYRAHVKGVHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                              224 NSPSHGGKFCEGSTRTLKLCNSQK--------CPRDSVDFRAAQC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 AEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCI 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 HS-----ISBNGTEHDG----ASRH 223
                                                                                                                            / Match 18.4%, Score 965.5; DB 5; Length 2165, Local Similarity 27.9%; Pred. No. 27.9%; Pred. Score 333; Indels 215, Massa 264, Conservative 114; Mismatches 333; Indels 215,
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FROATT, SWOOZO9; TSP1, 18.

PROSITE: PSSOO21, ADAM WEPRO; 1.

PROSITE; PSSOO32; TSP1, 15.

PROSITE; PSSOO142; ZINC_ROTHERS; 1.

SEQUENC: 2165 AA; 241397 MRA; PCC3DA8AAA9C4888 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boerboom D., Russell D.L., Richards J.S., Sirois J., "Coordinated Regulation of Transcripts Encoding ADAMTS-1 and Progesterone Receptor in Equine Preovulatory Follicles.", Submitted (AUG-2002) to the EWEL/GenBank/DDEJ databases. EMBL, AFS41975; AAN17331.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query March 18.0%; Score 944.5; DB 6; Length 7 Best Local Similarity 34.4%; Pred. No. 4.3e-75; Ratches 216; Conservative 83; Mismarches 242; Indels
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                                                                                                                                                                                                (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                              759 AA
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                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                              PRT;
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                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 -----YVFVVPVEVDSGGSYISHDILHHRKRRSAHGAS--NSLHYR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 IKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSVQTLPPE-DFCFYQGSLRSHRNSPS 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 VAVSTCAGLSGLIR-----TRDN-EFLISPLPQLLAQEHNYSSPAG-HHPHVLYKRTA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 EKRVRWYODYPG-----SQRTYPGHSPSHTPPASQSQEPEYSHRRWQKRHFC----- 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase 1 & II Team;
Analysis of the mouse transcriptome based on functional annotation of
No. 70 full length NNS.;
Netter 420:65-573 (2002).
REMBI, AROSE/97; BAC-9190.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%; Score 873.5; DB 11; Length 497;
39.2%; Pred. No. 4.9e-69;
tive 54; Mismatches 133; Indels 143; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 CALRAAGPGPPWGPAGLGRLAKALQLCCFCCASVAVALASDSGSSG--GSGLNDD----
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE 497 AA; 54372 MW; 3A72EDFC398BA2B9 CRC64;
                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical metalloprotease
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                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C578L/63; TISSUE-Cerebellum,
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                          PRT;
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                                                                          PRELIMINARY;
                                                                                                                                                                                                                              Mus musculus (Mouse)
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216 VETLVVADDKMAAFHG-TGLKRYLLTVMAAAAKAFKHPSIRNPVNLVVTRLVILGSGQEG 274
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                                    OBIGER 4, CONTRIBUTED 22, Created) 01-CCT-2002 (TrEMBLTED 22, Last sequence update) 01-CCT-2002 (TrEMBLTED 22, Last anotation update) 01-CCT-2003 (TrEMBLTED 23, Last annotation update) Similar to a distinciprin-like and metalloprotesse (reprolysin type) with thrombospondin type 1 motif, 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERIORS | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES | TROUBLES |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO27773; AAH27773.1; -...
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InterPro, IPR001590, Reprolysin.
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Matches 216; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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.Match
Local Similarity 34.4%, Pred. No. 1.3e-68;
Ces 216; Conservative 77; Mismatches 230, Indels 105; Gaps 23;
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EMELY 4.8083534; BAC38944.1; SEQUENCE 845.A3; 91239 MM; B496C3190D1A9225 CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                     891 EYSMPR-LGTEKOPPAOPSYTWAIVRSE 917
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Mus musculus (Mouse).
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MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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GENERAL INFORMATION:

APPLICANT: Friddia, carl Johan
APPLICANT: Friddia, carl Johan
APPLICANT: Hibbun, Erin
TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the
TITLE REPREDICE. LEX. 0219-188.

CURRENT PAPLICATION NUMBER: US 60/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FEASTSEQ for Windows Version 4.0
SEQ ID NO 4.0
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Copyright (c) 1993 - 2003 Compugen Ltd
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143;

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12   12   13   14   15   15   16   17   17   17   17   17   17   17	23 S.R.WELHAGELESSDACEDET - CANGROC. 350 YEGCLERKESLIESSPREELENSTLVVDERGAGNEHENITYVUTILANVSALFED. 271 YKSCLERKRSLLRSHRNEELANFELLVVDERGAGNHGHENITYTVLTILANVSALFED. 408	Db 391 ICSWKNEPCDTLGFAFISGWCSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 450 Qy 488 KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAG 524	A	
	Qy         608 GGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCBGSTR 667           Db         571 GGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGSVSHRSRLCTNFIN	QV         788 LYTKHHHTNOYYHNYTESGARSIRIYEMNYSSYISVBNALRRYYLNGHWTVDMPGRYK 847           Db         751 LYTKHHTNOYYHMYTESGARSIRIYEMNYSTSYISVRNALRRYYLNGHWTVDMPGRYK 810           QY         848 FSGTTFDYRRSYNEPRULATGFTNETIYELLFQORNPOYAMEYSMPRIGTGFORPAQD 907           Db         811 FSGTTFDYRRSYNEPRULATGFTNETIYELLFQGRNPOYAMEYSMPRIGTERQPPAQP 870           QY         908 SYTWALVRSECSVSCGGGR 926           QY         908 SYTWALVRSECSVSCGGGR 926           DD         811 SYTWALVRSECSVSCGGGC 899	SULT 2 Sequence 2, Application US/0993( Sequence 2, Application US/0993( Sextent No. 644338 Septicant: Friddle, Carl Johan APPLICANT: Friddle, Carl Johan APPLICANT: Friddle, Carl Johan APPLICANT: WILDU, Exin TILE REFERENCE: LEX-0219-UGA CURRENT APPLICATION NUMBER: US, CURRENT RILING DATE: 2010-09-109 FRIOR FPLING DATE: 2010-09-109 NUMBER OF SEQ ID NOS: 5 SOFTHARE: PASESEQ for Windows V TYPE: RAT TYPE: RAT TYPE: RAT	ORGANISM: homo sapiens US-09-30-672-2 Query Match 29.5%; Score 1543.5; DB 4; Length 491; Query Matches 333; Conservative 26; Mismatches 75; Indels 143; Gaps 13; Qy   MKPRARGWRGLAALWMLLAQVAEQVSPCRSHQRORRGSGQLEASPPRLLSRGPRRLTAWNS 60

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216 QGSLRSHRNSPSHGGKFCEGGTRTLKLCNSQKCPRDSVDFRAAQCAE-HNSRRFRGRHYK 274   1   1   1   1   1   1   1   1   1	GHENITIYVLTILANWYSALFKDGLMG	514 QYLHKPLSTAQAICLADQPKPVKEYKYPEKLPGBLYDANTQCKWQFGEKAKLCML	SRNVCIDGICERVQCDNVLGSDAVEDVGCVCNGNNSGCTIHRGLYTKHHETNQYTHNVTI SLDICINGECKHVGCDNVLGSDAREDRCKVCGGSSTCDALEGFRNDSLPRGCYNEVVQI PSGARGIRIYENNOSYSIKSVRALRRYYLLHI	RESULT 4  1S-09-159-154,7  1S-01-159-154,7  1S-01-159-154,7  1S-01-159-154,7  1S-01-159-154,7  1S-01-159-154,0  1S-01-159-154,0  1S-01-159-154,0  1S-01-159-154,0  1S-01-159-154,0  1S-01-159-159-159-159-159-159-159-159-159-15
00 00 00 00 00 00 00 00 00 00 00 00 00	6 6 6 6 6 6	5 8 5 8 5 8 5	2 5 2 5 2 5 2 5 2	RESULT 4 US-09-369-36, Sequence 7 PATENT NO. GENERAL IN APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT

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223 QOWRRPLARLHQRSVSKEKWCETLVVADARGVEYHGQPQVESYVLTIMMWVAGLFHDPS 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485 NMCKK--SEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQP-KPVKEYKYP 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 HDMWCRGGQCVKYCDEGPKPTHGHWSDWSSWSPCSRTCGGGGVSHRSRLCTNPKPSHGGKF 661
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                                                                                                                                                             129 DLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVA 188
                                                                                                                                                                                                                                         PGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNSPSHGG----KFCEGSTRTLKLCN 244
                                                                                                                                                                                                                                                                               104 PGFVSETRRRGGLGRAHIRAHTPACHILGEV----QDPELEGGLAAISACDGLKGVFQLSN 160
                                                                                                                                                                                                                                                                                                                          245 SOKC--PRDSVDFRAAQCAEH----NSRRFRGRHYKWKPYT---QVEADLCKLYCIAE 293
                                                                                                                                                                                                                                                                                                                                                                161 EDYFIEPLDSAPARPGHAQPHVVYKRQAPBRLAQRGDSSAPSTCGVQVYPEL----- 212
                                                                                                                                                                                                                                                                                                                                                                                                           294 GFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDEYKSC 353
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                                                                         Query Match 22.5%; Score 1179; DB 4; Length 997; BB EBET Local Similarity 10.18; Pred No. 11.5-95; Matches 292; Conservative 125; Mismatches 307; Indels 240;
TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-7
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RGGGVKACSLTSLAEGFNFYTERAAAVVDGTPCRPDTVDICVSGECKHVGCDRVLGSDLR 668
                                                                         EDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNA 828
                                                                                                         669 BDKCRVCGGDGSACETIEGVFSPASPGAGYEDVVWIPKGSVHIFIQDINLSLSHLALKGD 728
                                                                                                                                                                                        100 RDMDEAGNHRSQQTNTGTENQTLH-----VLTQXDLVSAYEVDHRGDYVSHEIMHHQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 RRRRAV------AVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 PRDSVDFRAAQCAEHNSRRPRGRHYKWKPYTQVEADLCKLYCIAEGFOFFFSLSNKVKDG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 TPGVNQTKFYSBEBRAELKHCFYKRLCQYQLRAHGRHQP------LLLKNEHK- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 RDLAEMG---SPDAAAAVRKDRLHPRQVKLLETLSEYEIVSPIRVNALGEPFPTNV-HFK 72
                                                                                                                                                        829 LRRYYLNGHWIVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTWFTLIVELLFQGRNPGV
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                                                                                                                                                                                                                                               889 AWEYSMPRIGTEKQPPAQPSYTWAIVR-SECSVSCGGG 925
                                                                                                                                                                                                                                                                         APPLICANT: Apte, Suncel
APPLICANT: Apte, Suncel
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding
FILE REFERENCE: 26473/4007/10-30-00
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION;
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US-09-369-364A-13
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NAME/KEY: MOD RES
LOCATION: (521)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 QTLPPEDFCPYQGSLRSHRNS--------PSHGGKPCEGSTRT 239
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                                                                                                                        Sequence 17, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneal
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
FILE OF INVENTION: Nucleic Acids Encoding Zinn
FILE REPRENCE: 26473/4007/10-30-00
CURRENT FILING DATE: 1999-08-06
KURRENT FILING DATE: 1999-08-06
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO. 17
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US-09-369-364A-17
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931 CGRG 934
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ore 984.5; DB 4; Length 967;
ed. No. 3.9e-79;
Mismatches 328; Indels 173; Gaps 35;
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                                                                                                                     SSCHNFGMIHDGEGNMCK----KSEGNIMSPTLAGRNG 504
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) NUMBER OF SEQ ID NOS: 14 ; SOFTWARE: Patentin version 3.0 ; SEQ LD NO 12 LENGTH: 727 ; TYPE: PRT ; ORGANISH: Nus sp. US-09-445-023A-12	Query Match 18.3%; Score 958.5; DB 4; Length 727; Best Local Similarity 35.3%; Pred No. 5.3e-77; Matches 222; Conservative 77; Mismatches 241; Indels 89; Gaps	Cy 371 VETLYNCKOM/ONIQHENITYYVITIANYSALEK	79 PEVTSNAALTLRNFCSWQKQHXSPSDRDPEHFDTAILFTRQDLCGSHTCDTLGMADVG 446 GMCSKYRSCTINEDTGLGLAFTIAHSGHHYDGGNWCKKSEGNIMSPTLA	Db 137 TVCDPSRSCSVIEDOCLQAAFTTAHELGHVPWPPHD-DAKHCASLNGVSGDSHLMASMLS 195  Qy 501 GRNGVPSWSPCSRQYLHKPLSTAQAICLADQPKPVKEYKPEKLPGELYDANTQCKWQFG 560  Db 196 SLDHSQPWSPCSAYWYTSFLDWGHGECLMDKPQWPIKLPSDLPGTLYDANRQCQFFFG 253	QY 561 EKAKLCMLDFKKDICKALWCHRIGKKCETKFWPAABGTICGHDWMCRGGQCVKYG 615	Qy 616 DEGPKPTHGHWSDWSSWSPCBRTCGGGVSHRSRLCTNPKPSHQGKPCEGSTRTLKLCN 673	QY 674 SQKCP-RDSVDFRAAQCAEHNSRRFRGRHYKWKP-YTQVEDQDLCKLYCIAEGFDF 727  1	Qy 728 FPSLSNKVXDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 787	Qy 788 LYTKHHTNQYYH-MVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVD 841 :	842 WPGR-YKESGTTFDYRRSYNEPENLIATG 	Qy 899 TEKQPPAQPSYT-WALVR-SECSV8CGGG 925	RESULT 10 US-09-445-023A-1 ; Sequence 1, Application US/09445023A ; Parent No. 5555856 ; GENERAL INPORMATION: ; APPLICANT: Hirose, Kunitaka	) APPLICANT: Insporati, Michinori ) APPLICANT: Hakozaki, Michinori ) APPLICANT: Tahida, Keiko ) APPLICANT: Tahida, Yukako ) APPLICANT: Tahida, Yukako ) APPLICANT: Tahida, Yukako ) APPLICANT: Tahida, Yukako ) APPLICANT: Matsushima, Kouji ) TITLE OF INVERTION: Composition and method of immunologically analyzing human ADAW ) FILE REPERBNCE: Q57092 ) CURRENT APPLICATION NUMBER: US/09/445,023A
264 NSRRFRGRHYKMKPYTQVBADLCKLYCIABGEDFFFSLSNKVKDGTPCSEDSRNVCIDGI 176KPRPPLQ	Db 198 CGVVDDEPRPTGKAETEDEDEGTEGEDEGFQWSPQDPALQGVGQFTGTGS-IRKKR-F 253  Qy 361 LRSHRNEELNVETLVVVDKKGMQNHGHENITTVLTILNMVSALFK	QY 407DGLMG	Cy 436 CDTLGFAP18GMCSKYRSCTINEDTGLGLAFTIAHESGHNFGMLHDGEGNMCKKSEG 492	551 ANTOCKROPCERKAKLOHLDEKKDICKALMCHRIGEKCETKEMPARETICHENDEREING 551 ANTOCKROPCERKAKLOHLDEKKDICKALMCHRIGEKCETKEMPARETICGHDMW 551 ANTOCKROPCERKAKLOHLDEKKDICKALMCHRIGEKCETKEMPARETICGHDMW 551 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 551 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 551 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 551 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 551 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 552 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 553 ANTOCKROPCHRIGEKCETKEMPARETICGHDMW 554 ANTOCKROPCHRIGEK	606 CRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGGVSHRSRLCTNPRPSHGGRFCE	664 GSTRTLKLCNSCKCP-RDSVDFRAAQCAEHNSRRFRGRHYKWKP-YTQVEDQDLCK   600 GKRYPKYSCKLEDCPDNNGTFREEQCHNESFSKASGSGAAZWEPKYAGVSPKRRKF	118 LYCIAEGEDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNG	Qy 778 NNSACTIHRGLYTKHHHTNQYYHWVIPSGARSIRIYEMNVSTSYISVRNALRRY 832	YLNGHWTUDMPGR-YKPGTTFDYRRYNBPENLIATGPTNFTLIVELLFQGRNPGVA 	WEYSMPRIGTERQPPAQPSYT-WAIVR-SECSUSC 922     :               YTYFVKKKKESFWAIPTPSAWVIEEWGECSKSC 370	RESULT 9 US-09-445-023A-12	Sequence 12, Application US/09445023A PREACH NO. 656586 GRERAL INFORMATION: APPLICANT: Hirose, Kunitaka APPLICANT: Horozeki, Michinori APPLICANT: Horozeki, Michinori APPLICANT: Horozeki, Michinori	APPLICANT: Island: INAMA AND AND AND AND AND AND AND AND AND AN

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473 KCGVCGGNGSTCKKISGSVIS--AKPGYHDIVIIPTGATNIEVKORNORGSRNNGSFLAI 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CG--SQTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHD-DAKQCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 KSEG-----NIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPRPVKEYKYPEK 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 LPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRK-----CETKFMPAAEGT 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               657 HGGKFCEGSTRTLKLCNSQKCP-RDSVDFRAAQCAEHN----SRRFRGRHYKWKP-YTQV 710
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APPLICANT: Lapiaer, Charles M.
APPLICANT: Lapiaer, Charles M.
APPLICANT: Lapiaer, Charles M.
APPLICANT: Lapiaer, Charles M.
APPLICANT: Excokep, Darwin J.
TITLE OF INVENTION: RECOMBINANT N.PROTEINASE,
TITLE OF INVENTION: AND THE FRODUCTION, WETHODS AND USES THEREOF KURNERS PODENCE ADDRESS:
ADDRESSED: Pennie & Edmonds, LLP
ADDRESSED:
                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                    17.8%; Score 934; DB 4; Length 727; 34.4%; Pred. No. 8.4e-75; tive 82; Mismatches 247; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                885 --NPGVAWEYSMPRLGTEKQPPAQPSYT-WAIVR-SECSVSC 922
CURRENT FILING DATE: 1999-12-03
PRICA PAPLICATION UNDERS: JP 9-160422
PRICK FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
LENGTH: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Best Local Similarity 34.4
Matches 221; Conservative
                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-491-522-11
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156 AVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFY 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.8%; Score 933; DB 4; Length 1205; Best Locat Similarity 28.9%; Pred No. 2.3-974; Andels 200; Matches 277; Conservative 125; Mismatches 356; Indels 200;
                                                                                                                                                    SOFTWARE: FastSEC for Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/441 con
FILING name.
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                                                                                                                                                                                                                                                                                                                                                                                                                                8389~0060-998
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                              NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 9399-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFRAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1205 amino acids
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                     ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POPOLOGY: linear
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                      USA
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                      COUNTRY;
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          STREET:
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á	Qy 527 CLADQPKPVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHR1GRK 586	US-09-491-522-5	1-522-5
ā	Ob 459 CLRDDPR-THDMPALEQLEYSNNBQCRFDFGLGYWMCTAFRTFDFCKQLMCSHPDNP 517	Query M	Query Match Best Local Similarity
ði -	CY 587CETKEMPAABCTICGHDWWCRCGGCVKYGDBGPKPTHGHWSDWSBWSPCSRTCGGGGVS 644	Matches	s 266; Conserv
ā	rkkgfplodimáapgkháfkáhátwitfdilk-RDĞ	õ	81 PERPASSSTR
8	Cy 645 HRSRLCINPRPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRFR 698	q	29 PPPPPANAR
ā	QCDNPHPANGGRTCSGLAYDF	<i>8</i>	141 DYVSHEIMHH
õ	Qy 699 GRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCS-EDSRNVCIDGICERV 757	ଷ	69 RLVSHVVSA
ā	Db 635HHWLPHEHRDAKERCHLYCESKETGEVVSMKRWYHDGTRCSYKDAFSLCVRGDCRKV 691	<i>*</i> ∂	185 SLVAPGFIVC
Ŏ.	Qy 758 GCDNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMYIPSGARSIRIYEMN 817	<u>ස</u>	129 RLVAPGATME
Q	Db 692 GCDGVIGSSKQEDKGCGVGGDNSHCKVVKGTFSRSFKKLGYIKMFEIPAGARHLLIQEAD 751	<i>&amp;</i>	245 SOKCPRDSVE
ò	Qy 818 VSTSYISVRN-ALRRYZLNGHWTVDWPGRYKFSGTTFDYRRSYNBPENLIATGPTNET 874	đ	187 EEFFIEPLEM
ä	Db 752 TTSHHLAVKNLETGKFILNEENDVD-PNSKTFIAMGVEWEY-RDEDGRETLQTMGPLHGT 809	8	303 NKVKDGTPCE
٥	QY 875 LIVELLEQG-RNPGVAMEYSMPRLGTEKQPPAQPSYTWAIVR-SECSVSCGGG 925	q _Q	222 GGPQP
Ω	DD 810 TTVLVIPRGDARISLTYKYMIHEDSLNVDDNNVLEDDSVGYEWALKKWSPCSKRCGGG 867	λ'o	363 SHRNBELNVE
Da.	RESULT 12	ପ୍	260 HAADDDYNEI
5		ð	412
	; bequence 5, ADDILCALLOH US/UM491842. ; Patent No. 6428988.	a a	320 LLSYGKSMSI
	4	ŏ	437 DTLGFAPISC
	APPLICANT: Laplers, Chaires M. APPLICANT: Proceedings of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr	ପ୍	375 GMQGYAPVTC
	; TITLE OF INVENTION: KECOMBINANT N-PROIETNABE, ; TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF , MIMBER OR ERMINEMEN.	ò	495 MSPTLAGRNC
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	PRIOR APPLIANTON NAMED DATA:	ପ୍	666 EVVSMKRMVF
	; AFFLICATION NUMBER: 00,000,533	ò	786 RGLYTKHHHI
	NIONKEY AGENI INFORMATION:  NAME: Banel B	ପ୍	1 :  : 726 KGTFTRSPKA
	** REPERTION NUMBER: 30,005 ** REPERTUCE/DOCKET NUMBER: 8389-0060-999 ** TELECOMMUNICATION INDOMETION:	۸٥ —	845 R-YKFSGTTE
	; TELECHION: 600-493-4935 : TELEPRY: And 403-546	<b>a</b>	: : : 786 KTFIAMGVEW
	99	ò	901 KQPPAQPS
	rics:	qa	845 DNNVLEEDSV
	; TYRNDENESS; single ; TOPOLOGY; linear	RESULT 13 US-09-130-491-13	3 0-491-13

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17.6%; Score 923; DB 4; Length 1211;

7. 28.6%; Pred. No. 1.86-7; Indels 168; Gaps 31;

rvairor 122; Mismatches 363; Indels 168; Gaps 31;
                                                                                                                                                                                                                                                                                               RGAAGLDGKGRDMDEAGNHRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRG 140
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271 GGGVOYTWRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNGKTPREEGCEAANBFSKA 330
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                                                                       APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 094.04/041001, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REPEIGNER: 094.04/041001, UNRBER: US/09/130, 491
CURRENT APPLICATION NUMBER: US 60/058, 108
EARLIER APPLICATION NUMBER: US 60/058, 108
EARLIER APPLICATION NUMBER: US 60/054, 961
EARLIER FILING DATE: 1997-08-06
EARLIER FILING DATE: 1997-08-06
SOFTWARE: PASTSEQ for Windows Version 3.0
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17.2%; Score 903; DB 4; Length 608;
Best Local Similarity 36.5%; Pred. No. 3.8e-72.
Marches 206; Conservative 73; Mismatches 236; Indels :
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Parent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
Sequence 13, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mus musculus
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342 CKWQHQHNQLGDDHEEHYDAAILFTREDLCG--HHSCDTLGMADVGTICSPERSCAVIED 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 YLHKPLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDI 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 CKALWCH--RIGRK-CETKFMPAAEGTICGHDMWCRGGQCVKYGDEGPK----PTHCHW 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           627 SDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRA 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 BQCBAKNGYQSDAKGVKTFVEWVPKYAGVLPADVCKLTCRAKGTGYYVVFSPKVTDGTEC 690
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                                                                                                                                                                                                                                                                                                                              Ouery Match

16.9%; Score 885.5; DB 4; Length 930;
Best Local Similarity 28.7%; Prec. No. 28e-70;
Matches 273; Conservative 120; Mismatches 354; Indels 205; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 ORRS-----GGLVHNIDQ--LYSG-----GGKVGYLVYAGGRR-----
APPLICANT: Hirohata, Satoshi Acids Encoding Zinc Metalloproteases. TITIE OF INVENTION: Nucleic. 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                          ORGANISM: mus musculus ADAMTS-5
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 930
                                                                                                                                                                                                                                                                                   US-09-369-364A-2
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50 EVQERAEPPGHPHPLAQRRRSKGLVQNIDQLYSGGGKVGYLVYAGGRR-FLLDLERDGSV 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GIAĞFVPAGGG-----DASPWRHRSHCFYRĞTV------DASPRSLAVF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 DLCGGLD-----GFFAVKHARYTLKPLLRGPWAEBEKGRVYGDGSARIIHVY-TREGFS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 -----TWWRRRRRRSISRARQ-----VELLLVADASMARLYG-RGLQHYLLTLASIAN 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KLCNSOKCPRDSVDFRAAQCAEHNSR.RFRG--.RHYKWKPYTQVEADLCKLYCIAEGFD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 FFFSLSNKVKDGTPCS------EDSRNVCIDGICELSVVSTSAHM-PQPPKED 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 -FEALPPRASCETPASTPEAHEHAPAHSNPSGRAALASQLLDQSALSPAGGSGPO---- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 ALF-----GLMGKDGTRH- 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645 HRSRLCTNPKPOHGGKPCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYK- 703
802 VIIPSGARSIRIYEMNVS----ISYISVRNALRRYYLNGHWTVDWPGR-YKFSGTTFDY 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 LFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVS 402
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                                                                                                         809 SGWSHRDDFLHGMGYSATKEILIVQIL--AIDPTKALGVRYSFFVPKKTTQK 858
                                                                                 856 RRSYNEPENLIATG -- PINETLIVELLFQGRNP---- GVAWEYSMPRLGTEK 901
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT ERISCIA HOPERS SQUIDD COMPANY
TITLE OF INVENTION: AGRECAN DECRADING METALLO PROTEASES
TILE REPERENCE: NOR509
CURRENT PILING DATE: 1998-07-24
NIMBER OF SGC ID NOS: 21
SOFTWARE; PREFEIL NOS: 21
                                                                                                                                                                                             RESULT 15
US-09-122-126B-15
Sequence 15, Application US/09122126B
Patent No. 6451575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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589 FAYRHCNNPAPRNNGRYCTGKRAIYRSCSLMPCPPNGKSFRHEQCEAKNGYQSDAKGVKT 648
                                        704 ---WKP-YTQVEDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGC 759
                                                                  649 FVEWVPKYAGVJ.PADVCKJ.TCRAKGTGYYVVFSPKVTDGTECRPYSNSVCVRGKCVRTGC 708
                                                                                                                          760 DNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVS 819
                                                                                                                                                     767 DQTRFTAYLALKKKNGEYLINGKYMISTSETIIDINGTVMNYSGWSHRDDFLHGMGYSAT 826
                                                                                                                                                                                                                                                                                                                             820 ----ISYISVENALRRYYLNGHWTVDWPGR-YKFSGTTFDYRRSYWEPENLIATG--PT 871
                                                                                                                                                                                                                                                                                                  872 NETLIVELLFQGRNP----GVAWEYSMPRLGTEK-------QPPAQPSYT---W 911
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Job time : 58 secs

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GenCore version 5,1.6
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OM protein - protein search, using sw model

October 28, 2003, 23:41:00; Search time 64 Seconds
(Without alignements)
2490:977 Million cell updates/sec

UG-09-981-151A-8 5216 1 WKPRARGWRGJAALWMLLAQ.......LEAACQPSATAYTALAFLES 952 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

629382 segs, 167460630 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:* Database :

Full State Applications. As: (1909)

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Pred. No. is the number of results predicted by chance to have a coors greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match I	Length DB	B	ID	Description
-	3846.5	73.5	1224	4	US-10-217-774-4	Sequence 4, Ap
C)	3846.5	73.5	1224	16	US-10-296-616-2	
m	2435.5	46.5	1221	12	US-10-240-545A-2	Sequence 2, Appl
4	2265	43.3	862	15	US-10-226-560-2	
S	1543.5	29.5	491	14	US-10-217-774-2	7
v	1391	26.6	959	10	US-09-788-043C-1	<b>,</b>
,	1390	26.5	908	10	US-09-963-791-2	N
00	1376	26.3	684	15	US-10-103-377C-2	2
σ	1319	25.2	757	10	US-09-963-791-24	24,
10	1257	24.0	1690	10	US-09-788-043C-5	'n
11	1243	23.7	1044	σ	US-09-858-081-9	4
12	1240	23.7	1104	12	US-09-842-469-2	Segmence 2, Appl:
13	1234	23.6	1133	σ	US-09-858-068-2	Sequence 2, Appl.
14	1222.5	23.3	1068	σ	US-09-858-081-2	Sequence 2, App
15	1211	23.1	1104	17	US-09-842-469-4	Sequence 4, Appl

61 PLFSAGTCVRHGTRSGSAWEPERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ 120

1 MKPRARGWRGLAALWMILAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS 60 

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121 TLHULTQYDLUSAYEVDHRGDYVSHEIMHQRRRRAVAVSEVESLHLRLKCPRHDFHMDL 180

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Sequence 12, Appl Sequence 5, Appli Sequence 7, Appli Sequence 3, Appli Sequence 2, Appli		occuence 14, Appr
US-09-858-081-12 US-09-918-171A-5 US-09-918-171A-7 US-09-918-171A-7 US-09-972-467-2	US-09-78 GA4C-7 US-09-918-171A-17 US-09-938-171A-17 US-09-938-171A-17 US-10-188-689-13 US-10-188-689-13 US-10-188-689-13 US-10-188-689-13 US-10-188-689-14 US-10-188-689-15 US-10-188-689-15 US-10-188-689-15 US-10-188-689-15 US-10-188-689-15 US-10-188-689-15 US-09-918-173-15 US-09-918-173-15 US-09-918-173-15 US-09-918-173-173-173-173-173-173-173-173-173-173	37-160-160-0T-80
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## ALIGNMENTS

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APPLICANT: Fiddle, Carl Johan
APPLICANT: Hilbur, Erin
TITLE OF INVENTION: Same US20020193583Alel Human Proteases and Polynucleotides Encod
TITLE OF INVENTION: Same US20020193583Alel Human Proteases and Polynucleotides Encod
TITLE OF INVENTION: Same US20020193583Alel Human Proteases and Polynucleotides Encod
TITLE OF INVENTION: Same US20020193583Alel Human Proteases and Polynucleotides Encod
TITLE OF INVENTION: USA0201936930, 972
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
SOOTWARE: PASSED FOR Windows Version 4.0
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                                      ; Sequence 4, Application US/10217774; Publication No. US20020193583A1; GENERAL INFORMATION:
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-----EYDLVSAYEVDHRGDYVSHEIMHQRRRRAVAVSEVESLHLRLKGSRHDFHVDL 112
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TITLE OF INVENTION: No. US2030129658Alei protease
FILE REPERBNCE: VO132PCT-664
CURRENT APPLICATION WUMBER: US10/296,616
CURRENT FAPLICATION WUMBER: 202-11-26
PRIOR APPLICATION WUMBER: UP 2000-393372
PRIOR FILING DATE: 2000-11-26
PRIOR FILING DATE: 2000-12-25
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                                                                                                                                                                                                                                             32 PAAAA-----PGSPSVPRPPPPAERPG-----WMEKG-----
                                                                             DB 16; Length 1224;
                                                                                                              73; Indels 143;
                                                                           73.5%; Score 3846.5; 75.4%; Pred. No. 0;
                                                                                                              Matches 738; Conservative 25; Mismatches
              TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 1224
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US-10-296-616-2
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Qy         682 VDFRAQCAEHISRRFRCR           :                                 Db         648 LDFRAQQCAEYISKFFRGW	QY         742 SEDSRNYCIDGICERVGCD           Db         708 SENKANDVCIDGOCELVGCD           QY         802 VITPSGARSIRIYBANYST           Db         768 VITPAGARSIRIYBANYST           QY         862 PENLIANGPRELIJUELL           QY         862 PENLIANGPRELIJUELL           QY         918 CSVSCGGG 925           QY         918 CSVSCGGG 925           DD         885 CSVSCGGG 925           PD         885 CSVSCGGG 925           RESULT 4         1	Sequence 2, Application US/1022; Sequence 2, Application US/1022; Publication No. US/2030050464A1; GENERAL INFORMATION; APPLICANT: Hu, Yi APPLICANT: Nepomnichy, Boris AppliCANT: Walter Nepomnichy, Boris	APPLICANT: Friddle, Carl Joha TILE OF INVENTION NO. US2003 FILE REPERRICE: LEX-0372-USA CURRENT APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR PILING DATE: 2001-08-22	FRIOR FILING DATE: 2001-07-27  PRIOR FILING DATE: 2001-07-27  PRIOR FILING DATE: 2000-07-28  NUMBER OF SEQ ID NOS: 6  SEQ ID NO 2  LENGTH: 862	TYPE: P. ORGANISS -10-226-5. Query Mat. Best Loca. Matches	85 47 145 78	OY 205 QTLPPEDFCEYQGSLRSHR.  Db 136 QK-PEVQQCFYQGSTRN1-  QY 261 AEHNSRRFRGRHYKWFPT  Db 187 QBHNYSSPAG-HHPHVLYK  QY 316 RNVCIDG  Db 239 RETEYHRRLQKQHFC
Qy 908 SYTWAIVRSECSVSCOGGR 926	RESULT 3 UG-10-240-545A-2 UG-10-240-545A-2 Sequence 2, Application US/10240545A Fublication No. US20030185828A1 GRNERAL INFORMATION: APPLICANT: Yamanouchi Pharmaccutical Co., Ltd. APPLICANT: Yamanouchi Pharmaccutical Co., Ltd. FILE REFERRENCE: 08959, 00002 CURRENT APPLICATION NUMBER: US/10/240,545A CURRENT APPLICATION NUMBER: PCT/10/11/033 FRIOR FILING DATE: 2002-10-02 FRIOR FILING DATE: 2002-11-18 NUMBER OF SEQ ID NOS: 26 SEQ ID NOS: 26 TENGTH: 1221 TYPE: RT.	US-10-240-545A-2 US-10-240-545A-2 Query Match Best Local Similarity 51.3%; Fred. No. 1.36-207; Matches 466; Conservative 110; Mismatches 195; Indels 129; Gaps 17;	Oy 85 ASSSTRGAAGLDGKGROMDEAGNHRSQOTNTGTENQTLHVLTQYDLVSAYEVDHRGDYVS 144	QY 205 QTLPPEDPCFYQGSLASHRNSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDFRAAQC 260  136 QK-PEVQCFYQGFIRND-SSSVAVSTGGLSGLIRTRKNBFLISPLQOLLA 186  QY 261 ABHNSRRFRGHYKKPYTQVBADLCKLYZIARGFPFFSLGNKVRGTPCSBDS 315	Qy         316 R	Oy 409	Qy         502 RNGVESNSPCSRQYLKRELSTAQAICLADDPKPVKEYKYPEKLPOELVDANTOCKWOFGE 561           468 NNGVESNSSCSRQYLKKELSTPQAGCLVDEPKQAGYKYPDKLPGQIYDADTOCKWOFGA 527           Qy         562 KAKLCMLDFKKDLCKALWCHRIGRKEFTKPMPAAEGTICGHDWMCRGQCKKYGDEGPKP 621           HILL

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30050464Alel Human Proteases and Polynuclectides Encod
DEAGNHRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYVS 144
                                                 DNVLGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHM 801
                                                                                                   TSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRRSYNE 861
                                                                                                                 ESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKSV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNSPSHGGKFCEGSTRTLKLCNSQ----KCPRDSVDFRAAQC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQVEADLCKLYCIAEGFDFFFSLSNKVKDG----TPCSEDS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRIAEBKIQRYRGYPG-----SGRNYPGYSPSHIPHASQS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soore 2265; DB 15; Length 862;
Pred. No. 1.2e-192;
07; Mismatches 194; Indels 122; Gaps
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CY 61 PLESAGTCVRHGTRSGGANEPERPASSTRGAAGLOGKGRDMDEAGNHRSQÇTNTGTENQ 120	Qy 121 TLHVLTQYDLVSAYEVDHRGDYVSHEIWHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDL 180	Qy 181 RTSSSLVARGFIVQTLGKTGTKKVQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTRTL 240	Oy 241 KLCNSOKCPRDSVDFRAAQCAEHNSRRFGRHYKNKPYTQVEA-DLCKLYCI 291 :	Qy 292 AEGFDFFESLSNKVKDGTPCSEDGRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE 349 :::     ::     ::     :	Cy 350 YKSCLRHKRELLRSHRNEELNVETLVVVDKKAMQHIGHENITTYVLILINNVSALFKD 407	QY 408	Qy 428 ICSWKNEPCDTLGFAPISGWCSKYRSCTINEDTGLGLAFTIAHESGHNFGWIHDCBGNWC 487	Qy 488 KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQ 524	RESULT 6 US-08-043C-1 Seniance 1 Annication HS/09988043C	parent No. UG2002010736131 parent No. UG2002010736131 parent No. UG2002010736131 parent No. UG2002010736131 parent No. UG2002010736131 parent No. UG2002010736131 parent No. UG2002010736131 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20020107361312 parent No. UG20070107361312 parent No. UG20070107312 parent No. UG20070107361312 parent No. U	Query Match 26.6%; Score 1391; DB 10; Length 959; Best Local Similarity 34.2%; Pred. No. 1.2e-114; Matches 308; Conservative 141; Mismatches 309; Indels 142; Gaps 24;	Qy 108 HRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYVSHEIMHHQRRRRAVAVSE 161
Oy 364 HRNEELAVETLVVVDKKAMQAHGHENITTYVLTILINNVSALFKDG	QY 409	Qy 442 APISGMCSKYRSCTINEDTGLGLAFIIAHESGHNFGMIHDGEGNMCKKSEGNIMSPTLAG 501	Qy 502 RNGVPSWSPCSRQYLHKFLSTAQAICLADQPRPVKEYKYFEKLPGELYDANTQCKWQPGE 561	Qy 562 KAKLCMLDPKKDICKALMCHRIGRKCETKFWPAABGTICGHDWNGRGGQCVKYGDBGPRP 621	Qy 622 THGHWSDHGSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCBGSTRTLKLCNSQKCPRDS 691	Qy 682 VDFRAAQCAEHNSREFRGRHYKWRPTQVEDQDLCKLYCLAEGFDFFSISNKVKDGTPC 741 5	Qy 742 SEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGIYTKHHFHPNQYYHM 801	Qy 802 VTIESGARSIRIYSMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFSGTTFDYRGYNE 861     :	Oy 862 PENLIATGFUNETLIVEL 879	RESULT 5 US-10-217-774-2 Sequence 2. Application US/1021774 Sequence 2. Application No. US202019363A1 Seguence 2. Application No. US2020219363A1 Seguence 2. Application No. US2020219363A1 Seguence 2. Application No. US2020219363A1 Septicant Friddle, Erin APPLICANT Friddle, No. US202019383A1el Human Proteases and Polynucleotides Encoding TITLE OF INVENTION: No. US202019383A1el Human Proteases and Polynucleotides Encoding TITLE OF INVENTION: No. US202019383A1el Human Proteases and Polynucleotides Encoding TITLE OF INVENTION: No. US202019383A1el Human Proteases and Polynucleotides Encoding TITLE OF INVENTION NUMBER: US/02/09-12 PRIOR PELING DATE: 2001-08-13 SPECIAL OF SEQ ID NOS: 5 SOFTWARE: Fasts of Er Windows Version 4.0 SENGEN: 491 STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE: PRT STYPE:	Query Match 29.5%; Score 1843.5; DB 14; Length 491; Best Local Similarity 57.7%; Pred. No. 1.1e-128; Matches 333; Conservative 26; Mismatches 75; Indels 143; Gaps 13;	OY 1 MKPRARGMRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQLEASPPRLLSRGPRRLTAMS 60 

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108 HRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYVSHEIMH--HQRRRRAV----AVSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 QGSIRSHRNSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDF-----RAAOCAEHNSRRFRG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 TGYLODORSTTKVALSNCVGLHGVI-----ATEDEEYFIEPLKNITEDSKHFSYENGH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 RHYKWKPYTQVBADLC-KLYCIAEGFDFFFSLSNKVKDGTP-CSEDSRNVCIDGICELSV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 PHVIYKKSALQQRHLYDHSHC-----GVSDFTRSGKPWWLNDTSTVSY----SLPI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 VSTSAHMPOPPKEDLFILPDEYKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 -----KDG----TRHDHALLLIGLDICSWKNEPCDTLGFAPISGMCSKYRSCTI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457 NEDIGLGLAFTIAHESGHNFGMIHDGEGNMC--KKSE-GNIMSPTLAGRNGVFSWSPCSR 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 OYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKD 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 ICKALWCHRIGRKCETKFMPAAEGTICG----HDMWCRGGQCVKYGDEGPKPTHGHWSDW 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 SSWSPCSKICGGGVSHRSKLCINPKPSHGGKFCEGSTRILKLCNSQKCPRDSVDFRAAQC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 SLWGECSRTCGGGVSSSLRHCDSPAPSGGGKYCLGERKRYRSCNTDPCPLGSRDPREKQC 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 VESLHLRIKGPRHDFHMDLRISSSLVAPGFIVQTLGKTGTKSVQTLPPE-----DFCFY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 VSKLFFKLSAXGKHFHLNLTLNTDFVSKHFTVEYMGKDG------PQWKHDFLDNCHY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 HSDHRLSYSSQBEFLTVLEHYQLTIPIRVDQNGAFLSFTVKNDKHSRRRRSMDPJDPQQA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 142;
                                                                                                                                                                                                                                                                                              Length 908;
                                                                                                                                                                                                                                                                                          Query Match 26.5%; Score 1390; DB 10; Best Local Similarity 34.2%; Pred. No. 1.4e-114; Matches 308; Conservative 141; Mismatches 309;
PRIOR FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                     US-09-963-791-2
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APPLICANT: TURNEY. C. ALexander Jr.
APPLICANT: TURNEY. C. ALexander Jr.
APPLICANT: Scalible, John
APPLICANT: Scalible, John
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Samds, Arthur Tr.
APPLICANT: Samds, Arthur Tr.
APPLICANT: Samds, INC.
APPLICANT: US.
CURRENT SAMDS INC.
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,769
PRIOR APPLICATION NUMBER: US 60/169,769
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            162 VESLHLRIKGPRHDFHMDIRTSSSIVAPGFIVQTLGKTGTKSVQTLPPE-----DFCFY 215
                                                216 QGSLRSHRNSPSHGGKFCEGSTRTLKLCNSQKCPRDSVDF----RAAQCAEHNSRFFG 270
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Patent No. US20020120113A1
GENERAL, INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 QK-PEVQQCFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNBFLISPLPQLLAQBHNHSS 193
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PUBLICATION NO. US20030073098A1
SENERAL INFORMATION: US20030073098A1
SENERAL INFORMATION: US2003007309A1
TITLE OF INVENTION: 65577, A Human Matrix
TITLE OF INVENTION: Metallopxoteinase and Uses Therefor FILE REPERRORE: M7010-409PIRMN
CURRENT PELICATION NUMBER: US/10/103,377C
CURRENT PELICATION NUMBER: 602-82-26
FRIOR PILING DAME: 2001-03-23
PRIOR FILING DAME: 2001-03-23
NUMBER OF SEQ ID NOS: 7 AND SEQ ID NOS: 7 AND SECONO 100: 7 SOFTWARE: PASSED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 -----
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-10-103-377C-2
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| Sequence 24, Application US/09963791 |
| Paretr No. US20202012013A1 |
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| GENERAL INVORMATION: |
| APPLICANT: Donoiso, Gregory |
| APPLICANT: Purner, C. Alexander Jr. |
| APPLICANT: Securits, Glenn |
| APPLICANT: Securits, Arthur T. 20. |
| APPLICANT: Sands, Arthur T. 20. |
| APPLICANT: Sands, Arthur T. 20. |
| TITE OF INVERTION: No. US20202120113A1e1 |
| Human Proteases and Polynucleotides Encody |
| FILE REFERENCE: LEX-0.105-105 |
| CURRENT FILING DATE: A00012.08 |
| PRIOR APPLICATION NUMBER: US 601.12-09 |
| PRIOR FILING DATE: A999-12-09 |
| PRIOR FILING DATE: A999-12-09 |
| NUMBER OF SEQ ID NOS: 25 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO. |
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355 RHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDGLMG--- 411
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                               440 SGGGKYCLGERKRYRSCNTDPCPLGSRDFREKQCADFDNMPFRGKYYNWKPYTGGGVKP- 498
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552 NTOCKWOFGEKAKLCMLDFKKDICKALWCHRIGRKCETKFMPAAEGTICGHDMWCRGGQC 611
                                                                                                                                                                                                          532 VPVGFR-PEAVDGGMSGWSAWSICSRSCGMGVQSAERQCTQPTPKYKGRYCVGERKRFRL 590
                                                                                                                                                                                                                                                                                        672 CNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFFSL 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                   790 TKHHHTNQYYHNVTIPSGARSIRIXBMNVSTSYISVRNA-LRRYYLNGHWTVDWPGRYKF 848
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417 FIMSPQLLYDAAPLTWSRCSRQYITRFLDRGWGLCLDDPPAKDIID--FPSVPPGVLYDV 474
                                                                                                              475 SHOCRLOYGAYSAFC--EDMONVCHTLWC-SVGTTCHSKLDAAVDGTRCGENKWCLSGEC 531
                                                                                                                                                                       612 VKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEGSTRTLKL 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09858081
Patent No. US20020072490A1
GENERAL INFORMATION:
APPLICANT: Kapellor-Libermann, Rosana
APPLICANT: Roblid-William James
APPLICANT: Roblid-William James
IITLE OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE
TITLE OF INVENTION: FPAMILY MENGER AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/858,081
CURRENT FILING DATE: 2000-05-15
RRIOR APPLICATION NUMBER: 60/204,159
RRIOR FILING DATE: 2000-05-15
RRIOR APPLICATION NUMBER: 60/204,160
RRIOR FILING DATE: 2000-05-15
RRIOR FILING DATE: 2000-05-15
NUMBER: OF SEQ. ID NOS: 14
SOFTWARE: RESESEO FOR Windows Version 4.0
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 295; Conserva
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US-09-858-081-9
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Patent No. US20020107361A1

GENERAL INFORMATION:

APPLICANT: ALO, Fengrong

APPLICANT: ALO, Fengrong

APPLICANT: ALO, Fengrong

TITLE OF INVENTION: No. US20020107361A1e1 Metalloproteases Having

TITLE OF INVENTION: Phrombspondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Phrombspondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Phrombspondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Thrombspondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: Thrombspondin Domains and Nucleic Acid Compositions

TITLE OF INVENTION: 2001-02-16

CURRENT PAPLICATION NUMBER: US/09/188, 043C

CURRENT PAPLICATION NUMBER: 02/01-02-16

PRIOR PILING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 10

CONTANTE PRIOR PRIOR DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 10
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Best Local Similarity 34.1%; Pred. No. 2.6e-102;
Matchee 293; Conservative 128; Mismatchee 313; Indels 126; Gaps 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 EDYFIEPLDSAPARPGHAQPHVV-----YKROAPER--------LA 197
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                                                                                                                                                                                                              619 GAWTIDWPRKEDVAGTAFHYKRFTDEPESLEALGPISBNJ.VMVLLQEQNLGIRYKENVP 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 PGFVSETRREGLGRAHIRAHTPACHLLGEV---QDPELEGGLAAISACDGLKGVFQLSN 164
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          499 CALNCLAEGYNFYTERAPAVIDGTQCNADSLDICINGECKHVGCDNILGSDAREDRCRVC 558
                                                               776 NGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLN 835
                                                                                                                                                                                                                                                                                            896 -- RIGIEKQPPAQPSYTWAIVR-SECSVSCGGR 926
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ORGANISM: human
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LENGTH: 1690
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84 PASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYV 143
                                                                                                                   144 SHEIMHHORRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKS 203
                                                                                                                                           204 VQTLPPEDFCFYQGSLRSHRNS-----------PSHGGKFCEGSTR 238
                                                                                                                                                                                                                                      115 QRAARPH--CLYAGHLQGQASTSHVAISTCGGLHGLIVADEEEYLIEPLHGGP--KGS-- 168
                                                                                                                                                                                                                                                                             239 TLKLCNSQKCPRDS----VDFRAAQ------CAEHNSRRFRGRHYKWKPYTQVEADLC 286
                                                                                                                                                                                                                                                                                                   169 ------RSPEESGPHVVXKRSSLRHPHLDTACGVRDEKPWKGRPWWLRTLKPPPAR-- 218
                                                                                                                                                                                                                                                                                                                                                         287 KLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSÆHMPQPPKEDLFIL 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 BSSLGSTVNILVTRLILLTEDQPTLEITHHAGKSLDSFCKWQKSIVNHSGHGNAIPENGV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 TRHDHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTJAHESGH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   475 NFGMIHDGEGNMC---KKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQ 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      768 VEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNVSTSYISVRN 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828 ALRRYYLNGHWTVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPG 887
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                                                                  3 PACOILEMWALAL-GLGLMFEVTHAFRSQ------DEFLSSLESYEIAFPTRVDHNGALL 54
                                                                                                                                                                                                                                                                                                                                                                                                294; Conservative 134; Mismatches 317; Indels 194; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888 VAMEYSMPRLGTEKOPPAOPSYTWAIVR-SECSVSCGGG 925
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US-09-858-068-2
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84 PASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 KLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFIL 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 PACQILRWALAL-GLGLMFEVTHAFRSQ------DEFLSSLESYEIAPPTRVDHNGALL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 SHEIMHHQRRRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 ORAAR PH -- CLYAGHLOGQASSSHVAISTCGGLHGLIVADEEEYLIEPLHGGP -- KGS -- 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
23.6%; Score 1234; DB 9; Length 1133;
Best Local Similarity 30.3%; Pred. No. 166-100;
Matches 310; Conservative 138; Mismatches 332; Indels 244; Gaps
                     APPLICANT: Silos-Santiago, Inmeculada
TITLE OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE
TITLE OF INVENTION: FALLY MEMBER AND USES THEREOF
                                                                                          FILE REPERRNCE: 10448-05701
CURRENT APPLICATION NUMBER: US/09/88,068
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 06/204,159
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARR: FastSEQ for Windows Version 4.0
LENGTH: 1133
Cook, William James
                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-858-068-2
   APPLICANT:
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ò	711 EDQDLCKLYCIAEGFDFFFSLSNKVKDGTPCSEDSRNVCIDGICERVGCDNVLGSDAVED 770
QQ	694 GGVKACSLICTAEGENFYTERAAAVDGTPCREDTVDICVSGECKHVGCDRVLGSDLRED 753
ò	VCGVCNGNNSACTIHRGLYTKHHHTNQYYHMYTIPSGARSIRIYEMNVSTSYISVRNALR
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õ	RYYLNGHWIVDGRYKFSGTIFDYRRSYNEPENLIATGPINETLIV
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අ	NRLHAILPLAAAPFLQVLARTELPALRYRFNAP-IARDSLPPYSWHYAPWT
õ	922 CGG 92S 
DP	929 CAGG 932
RESULT 14 US-09-858-0	14 58-081-2 nce 2, Application US/09858081
; Patent ; GENERA	), US20020072490A1 INFORMATION: IT, Vanellar:
; APPLI ; APPLI ; APPLI	aga g
; TITLE	OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE OF INVENTION: FAMILY MEMBER AND USES THEREOF
CURRENT	KEFEKENUE: 10444-043001 TAPLICATION NUMBER: US/09/858,081 NUT ETITUC DAME: JOHLAGE
	APPLICATION NUMBER: 60/204,15 FILING DATE: 2000-05-15
PRIOR	APPLICATION N FILING DATE:
SOFTWARE; SEQ ID NO 2; LENGTH: 1	astSEQ for W
	TYPE: PRYT ORCANISM: Womc sapiens .09-858-081-2
Query Ma Best Loc Matches	/ Match Local Similarity 30.6%; Pred. No. 1.6e-99; Conservative 133; Mismatches 315, Indels 221; Gaps 25;
ò	84 PASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQTLHVLTQYDLVSAYEVDHRGDYV 143
ДQ	
ð	144 SHEIMHHORRRAVAVSEVESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTLGKTGTKS 203
ପ୍ପ	RRGTGATAESRLFYKVASPSTHFLL
ò	204 VQTLPPEDFCFYQGSLRSHRNSPSHGGKFCEGSTR 238
Ор	115 QRAARPHCLYAĞHLQGQASSSHVAISTCGGLHGLIVADEBEYLIEPLHĞĞPKĞS 168
ò	239 TLKICNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVBADLC 286
q _Q	169RSPEESGPHVYYKRSSLRHPHLDTACGVRDEKPWKGRPWNLRTLKRPPPAR 218
ò	287 KLYCIAEGEDFFFSLSNKVKDGTPCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFIL 346
අු	219PLGNETERGQPGL
è	347 DDRVKCT DUVDQT I DQUDMBBI NINFTI MAMANHADDAT TATAMAYCA). DV 406

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                                                                                                                                                                                                                                                                                                                                                                                                                  475 NFGMIHDGEGNMCKKSEGNIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKP 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 TFGMNHDGVGNSC--GAPKLMAAHITMKTNPFVWSSCSRDYITSFLDSGLGLCLNNRP-P 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 VKEYKYPEKLPGELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRKCETKFMPA 594
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                                                                                                                                                          277 DSSLGSTVNILVTRLILLTEDQPTLEITHHAGKSLDSFCKWQKSIVNHSGHGNAIPENGV 336
                                                                                                                                                                                                                                                                                                                                                          415 TRHDHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRSCTINEDTGLGLAFTIAHESGH 474
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SEQUENCE 4, APPLICATION NO. 10270030166899A1

GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: ADAPTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
TITLE OF INVENTION: ADAPTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
TITLE OF INVENTION: ADAPTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
TITLE OF INVENTION: ADAPTS 101093B
CURRENT FILING APPE: 2001-04-26

NUMBER OF SEQ ID NOS: 9.1
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23.1%; Score 1211; DB 12; Length 1104;
Best Local Similarity 31.6%; Precd. No. 1.7e-98,
Marches 285; Conservative 131; Mismatches 344; Indels 142; Gaps
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117 TENQTLHVLTQYDLVSAYEVDHRGDYVSHEIMHQRRRRAVAVSEVESLHLRLKGPRHDF 176

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88 LLNLTRSPRLLAGHVSVEYWTREGLAWQRA.-ARAHCLYAGHLQGQAGS-SHVAVSTCGG 144
                                                                                                                                                                                                                                                                                                           237 TRILKLCNSQKC-----PRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEADLCKL 288
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